

FULL-LENGTH cDNA

FIELD OF THE INVENTION

The present invention relates to polynucleotides encoding
5 novel polypeptides, the polypeptides encoded by these
polynucleotides, and new uses of these.

BACKGROUND OF THE INVENTION

The genomic DNAs of various living organisms are currently
10 being sequenced and analyzed all over the world. The entire
genomic sequences of more than 40 species of prokaryotes, a
lower eukaryote, yeast, a multicellular eukaryote, *C. elegans*,
and a higher plant, *arabidopsis*, and such have already been
determined. Analysis of the human genome, presumed to have
15 three billion base pairs, was advanced under global cooperative
organization, and a draft sequence was disclosed in 2001. In
2003 the complete structure had been elucidated and publically
disclosed. A genome is a blueprint for highly complicated
living organisms. The aim in determining a genomic sequence is
20 to reveal the function and regulation of all genes, and to
understand living organisms as a network of interactions between
genes, proteins, cells or individuals. Understanding living
organisms through the genomic information of various species is
not only academically important, but also socially significant
25 from the viewpoint of industrial application.

However, simply determining a genomic sequence will not
reveal the function of all genes. For example, in the case of
yeast, the function of only approximately half of the 6000 genes
predicted on the basis of genomic sequence have been deduced.
30 The human genome has been estimated to contain about 30,000 to
40,000 genes. Further, 100,000 or more types of mRNAs are said
to exist when variants produced by alternative splicing are
taken into consideration. Therefore, it is desirable to
establish "a high throughput system for analysis of gene
35 functions" which allows rapid and efficient identification of

the functions of vast amounts of genes obtained by genomic sequencing.

Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to correctly predict the structure of an encoded protein based solely on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows easy identification of the protein's primary structure. In human cDNA research to date, more than three million ESTs (Expression Sequence Tags) are publicly available, which presumably covers no less than 80% of all human genes.

EST information is utilized in a variety of ways, for example in analyzing the structure of the human genome, or in predicting exon regions of genomic sequences or their expression profiles. However, most human ESTs have been derived from regions proximal to the cDNA 3'-end, and little information is available from around the mRNA 5'-end. In human cDNAs, the full-length protein sequence of approximately 15,000 corresponding mRNAs have been deduced.

It is possible to identify the mRNA transcription start site on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA contained in that sequence, or in the regulation of its expression at the translation stage. Also, since the atg codon, or translation start site, is contained in the 5'-region of a full-length cDNA, translation to proteins will occur in the correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA, or to analyze the biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of full-length cDNA provides valuable information which complements genome sequencing information. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

Therefore, if a novel human full-length cDNA can be isolated, it can be used for developing medicines for diseases in which its gene is involved. A protein encoded by such a gene can be used as a drug by itself. Thus, obtaining full-length
5 cDNAs encoding novel human proteins is of great significance.

In particular, human secretory proteins or membrane proteins would be useful used as medicines in the same manner as tissue plasminogen activator (TPA), or as target proteins for medicines like membrane receptors. In addition, genes for
10 signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, and such, are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human
15 diseases have been elucidated.

Isolating novel full-length human cDNA clones, only a few of which have been isolated, is of great significance. The isolation of novel cDNA clones encoding secretory proteins or membrane proteins is especially desired since such proteins
20 would be useful in themselves as medicines, and also their clones would potentially include genes involved in disease. In addition, genes encoding proteins involved in signal transduction, glycoprotein, transcription, or disease, are expected to be useful as target molecules for therapy, or as
25 medicines in themselves. These genes form a gene group predicted to be strongly involved in disease. Thus, identification of full-length cDNA clones encoding these proteins has great significance.

SUMMARY OF THE INVENTION

An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

The inventors have developed a method for efficiently
35 cloning, from a cDNA library having a very high fullness-ratio, human full-length cDNAs predicted to be full-length cDNA clones,

where that cDNA library is synthesized by an improved method (WO 01/04286) of oligo-capping (K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)). The nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-end, and, if required, from their 3'-end.

Among the clones obtained, representative clones estimated to be novel and full-length were analyzed for their full-length nucleotide sequence. The determined full-length nucleotide sequences were analyzed using a BLAST homology search of the databases shown below. Homology searches of the present invention were carried out based on full-length cDNA information, including the entire coding region, and thus homology to every part of a polypeptide could be analyzed. Therefore, in the present invention, the reliability of homology searches has been greatly improved.

[1] SwissProt

(http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html),

[2] GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>),

[3] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (<http://www.rcsb.org/pdb/index.html>), PIR (<http://pir.georgetown.edu/pirwww/pirhome.shtml>), and PRF (<http://www.prf.or.jp/en/>); overlapping sequences have been removed.), and

[4] RefSeq (<http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>).

The gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

In the present invention, gene functions were revealed by analysis of expression profiles *in silico*, based on full-length nucleotide sequence information. The expression profiles used

in the expression frequency analysis were studied based on databases containing a sufficient amount of fragment sequence data. Expression frequency analysis was carried out by referring, for these expression profiles, to the full-length
5 nucleotide sequences of the many cDNA clones obtained in the present invention. Thus, highly reliable analysis was achieved by referring to the full-length nucleotide sequences of a wide variety of genes in a sufficiently large population for analysis (expression profiles). Namely, the results of expression
10 frequency analysis using the full-length sequences of the present invention more precisely reflect gene expression frequency in tissues and cells from which a certain cDNA library was derived. Thus, the full-length cDNA nucleotide sequence information of the present invention made it possible to achieve
15 highly reliable expression frequency analysis.

The full-length cDNA clones of the present invention were obtained by a method comprising the steps of [1] preparing libraries containing cDNAs with a high fullness ratio using oligo-capping, and [2] assembling 5'-end sequences and selecting
20 those with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction). The use of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable full-length cDNAs to be readily obtained
25 without using such special techniques. Primers, which are designed for use in obtaining cDNAs capable of being expressed, are not limited to the 5'- and 3'-end sequences of a polynucleotide.

Specifically, the present invention relates to
30 polynucleotides and proteins encoded by the polypeptides as follows.

[1] A polynucleotide selected from the group consisting of:
(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence according to any one of SEQ ID NOs: 1-
35 1956 and SEQ ID NOs: 3913-3951;

(b) a polynucleotide comprising the nucleotide sequence encoding a polypeptide that comprises the amino acid sequence of any one of SEQ ID NOs: 1957-3912 and SEQ ID NOs: 3952-3990;

5 (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide, which comprises the amino acid sequence selected from SEQ ID NO: SEQ ID NOs: 1957-3912 and SEQ ID NOs: 3952-3990 wherein one or more amino acids have been substituted, deleted, inserted, and/or added, and which is functionally equivalent to the polypeptide comprising the selected amino acid
10 sequence as described above;

(d) a polynucleotide which hybridizes to a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951, and which comprises the nucleotide sequence encoding a polypeptide functionally
15 equivalent to a polypeptide encoded by the selected nucleotide sequence as described above;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotides according to any one of (a)-(d);

20 (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951; and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any
25 one of SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951.

[2] A polypeptide encoded by the polynucleotide according to [1], or a partial peptide thereof.

[3] An antibody which binds to the polypeptide or the peptide according to [2].

30 [4] An immunoassay method for the polypeptide or the peptide according to [2], which comprises the steps of:

(a) contacting the polypeptide or the peptide according to [2] with the antibody according to [3]; and

(b) observing the binding between the two.

35 [5] A vector comprising the polynucleotide according to [1].

[6] A transformant comprising the polynucleotide according to [1] or the vector according to [5].

[7] A transformant which comprises the polynucleotide according to [1] or vector according to [5] in an expressible manner.

[8] A method for producing the polypeptide or the peptide according to [2], which comprises the steps of:

- (a) culturing the transformant according to [7]; and
- (b) recovering the expression product.

[9] An oligonucleotide comprising 15 or more nucleotides, which comprises the nucleotide sequence according to any one of SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951, or a nucleotide sequence complementary to the complementary strand thereof.

[10] A primer for synthesizing a polynucleotide, which comprises the oligonucleotide according to [9].

[11] A probe for detecting a polynucleotide, which comprises the oligonucleotide according to [9].

[12] A polynucleotide according to any one of:

(a) an antisense polynucleotide comprising a nucleotide sequence complementary to the transcript of the polynucleotide according to [1];

(b) a polynucleotide with the ribozyme activity for specifically cleaving the transcript of the polynucleotide according to [1]; and

(c) a polynucleotide which downregulates the expression of the polynucleotide of [1] due to RNAi activity in a host cell.

[13] A method for detecting the polynucleotide according to [1], which comprises the steps of:

(a) incubating a target polynucleotide with the oligonucleotide according to [9] under conditions ensuring hybridization; and

(b) detecting the hybridization between the target polynucleotide and the oligonucleotide according to [9].

[14] A database of polynucleotides and/or polypeptides, which comprises information on at least one of the nucleotide sequences of SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951 and/or

on at least one of the amino acid sequences of SEQ ID NOs: 1957-3912 and SEQ ID NOs: 3952-3990.

Herein, "polynucleotide" is defined as a molecule, such as a DNA or RNA, in which multiple nucleotides are polymerized. There is no limitation as to the number of polymerized nucleotides. If a polymer contains a relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotides or oligonucleotides of the present invention can be natural or chemically synthesized. Alternatively, they can be synthesized using a template polynucleotide in an enzymatic reaction such as PCR. Furthermore, the polynucleotides of the present invention may be modified chemically. Single-stranded and double-stranded polynucleotides are included in the present invention. In this specification, especially in the claims, when the polynucleotides are described merely as "polynucleotide", it means not only single-stranded polynucleotides but also double-stranded polynucleotides. When it means a double-stranded polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the corresponding complementary strand is essentially determined.

All the cDNAs provided by the present invention are full-length cDNAs. "Full-length cDNAs" herein means cDNAs containing the ATG codon, which is the start point of translation therein. Untranslated regions upstream and downstream of the protein-coding region are both naturally contained in natural mRNAs and are not essential. It is preferable that the full-length cDNAs of the present invention contain a stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the restriction map of the vector pME18SFL3.

DETAILED DESCRIPTION OF THE INVENTION

All of the clones (1,995 clones) of the present invention are novel and encode full-length polypeptides. Further, all of the clones are cDNAs with a high fullness ratio, and which were obtained by oligo-capping method. None of the clones are identical to any known human mRNAs (namely, they are novel clones) selected by searching 5'-end sequences and mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene (Human) (<http://www.ncbi.nlm.gov/UniGene>) databases using BLAST homology [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]. They are also clones that were assumed to have a higher fullness ratio among members in assembled clusters. Most of the clones with a high fullness ratio in a cluster had nucleotide sequences longer in the 5'-end direction.

All of the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on 5'-end and 3'-end sequences, or using primer sets of primers designed based on 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of 1,995 full-length cDNA clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rules set out in "DDBJ/EMBL/GenBank Feature Table Definition" (<http://www.ncbi.nlm.nih.gov/collab/FT/index.html>). The start position number corresponds to the first letter of "ATG", the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated by flanking with the mark "...". However, in clones without a stop codon, the termination position is indicated by the mark ">", according to the above rules.

Table 1

	Clone Name	SEQ ID NO of Nucleotide	CDS Portion	SEQ ID NO of Amino Acid
5	3NB692004045	1	220..>1437	1957
	ADIPS2000069	2	48..1538	1958
	ADRGL2010315	3	1182..1604	1959
10	ADRGL2010594	4	203..664	1960
	AHMSC1000138	5	135..455	1961
	ASTRO2008972	6	455..805	1962
	ASTRO2015162	7	244..951	1963
	ASTRO2016114	8	796..1779	1964
15	ASTRO3000154	9	2154..2807	1965
	BEAST2000981	10	149..1357	1966
	BLADE2000256	11	461..1687	1967
	BLADE2001031	12	27..506	1968
	BLADE2002310	13	1065..>2616	1969
20	BLADE2002744	14	82..510	1970
	BLADE2004849	15	276..1202	1971
	BLADE2006043	16	218..622	1972
	BLADE2007735	17	310..723	1973
	BLADE2007744	18	1629..>1944	1974
25	BLADE2007799	19	917..2158	1975
	BLADE2008809	20	286..1575	1976
	BRACE1000475	21	2878..3471	1977
	BRACE2002392	22	76..1008	1978
	BRACE2003628	23	145..1164	1979
30	BRACE2005991	24	337..666	1980
	BRACE2010336	25	23..1387	1981
	BRACE2012528	26	114..1289	1982
	BRACE2012625	27	84..1406	1983
	BRACE2012833	28	244..651	1984
35	BRACE2012838	29	127..468	1985
	BRACE2012936	30	617..994	1986

	BRACE2012947	31	756.. 1223	1987
	BRACE2013009	32	777.. 1487	1988
	BRACE2013126	33	334.. 651	1989
	BRACE2013132	34	73.. 795	1990
5	BRACE2016896	35	27.. 1298	1991
	BRACE2017359	36	755.. 1228	1992
	BRACE2017397	37	99.. 872	1993
	BRACE2017580	38	514.. 834	1994
	BRACE2017844	39	1674.. >2015	1995
10	BRACE2017872	40	148.. >1404	1996
	BRACE2017992	41	934.. 1245	1997
	BRACE2019348	42	1423.. 2004	1998
	BRACE2023633	43	122.. 478	1999
	BRACE2023744	44	349.. 771	2000
15	BRACE2025452	45	55.. 426	2001
	BRACE2026404	46	67.. 408	2002
	BRACE2027312	47	255.. 848	2003
	BRACE2027382	48	1749.. 2090	2004
	BRACE2028956	49	133.. 480	2005
20	BRACE2030039	50	87.. 719	2006
	BRACE2032584	51	129.. 485	2007
	BRACE2033128	52	296.. 676	2008
	BRACE2034434	53	1963.. 2664	2009
	BRACE2035120	54	22.. 1938	2010
25	BRACE2035191	55	207.. 542	2011
	BRACE2039362	56	81.. 440	2012
	BRACE2039607	57	1850.. 2398	2013
	BRACE2042541	58	96.. 1562	2014
	BRACE2046976	59	836.. 1345	2015
30	BRACE2047232	60	1434.. 2363	2016
	BRACE2047975	61	299.. 652	2017
	BRACE3001403	62	1965.. 2507	2018
	BRACE3001973	63	24.. 2702	2019
	BRACE3002264	64	72.. 2870	2020
35	BRACE3002344	65	113.. 3295	2021
	BRACE3002541	66	2255.. 2593	2022

	BRACE3002756	67	595.. 2700	2023
	BRACE3003866	68	2667.. 3542	2024
	BRACE3004046	69	2774.. 3277	2025
	BRACE3004371	70	467.. 832	2026
5	BRACE3004767	71	3944.. 4390	2027
	BRACE3004887	72	2217.. 2792	2028
	BRACE3004981	73	3154.. 3624	2029
	BRACE3005870	74	5.. 379	2030
	BRACE3005903	75	328.. 3378	2031
10	BRACE3006553	76	2589.. 3344	2032
	BRACE3007649	77	4951.. 5472	2033
	BRACE3007869	78	932.. 1549	2034
	BRACE3009075	79	1318.. 2025	2035
	BRACE3009265	80	1886.. 2374	2036
15	BRACE3009392	81	2134.. 3072	2037
	BRACE3009416	82	2056.. 2805	2038
	BRACE3009539	83	117.. 449	2039
	BRACE3010702	84	1062.. 1619	2040
	BRACE3011447	85	289.. 786	2041
20	BRACE3011774	86	906.. 1331	2042
	BRACE3013418	87	17.. 3121	2043
	BRACE3013874	88	765.. 2255	2044
	BRACE3013986	89	335.. 661	2045
	BRACE3014523	90	318.. 1532	2046
25	BRACE3014714	91	1034.. 2182	2047
	BRACE3015090	92	287.. 616	2048
	BRACE3015898	93	119.. 448	2049
	BRACE3016020	94	62.. 586	2050
	BRACE3016167	95	67.. 507	2051
30	BRACE3016580	96	225.. 578	2052
	BRACE3016788	97	1740.. 2486	2053
	BRACE3016810	98	2064.. 2561	2054
	BRACE3016862	99	33.. 335	2055
	BRACE3017253	100	86.. 1342	2056
35	BRACE3018083	101	1447.. 2541	2057
	BRACE3019570	102	320.. 3358	2058

	BRACE3019611	103	2005.. 2484	2059
	BRACE3019817	104	7.. 345	2060
	BRACE3019941	105	1120.. 3507	2061
	BRACE3020356	106	344.. 661	2062
5	BRACE3020669	107	2192.. 2650	2063
	BRACE3021430	108	243.. 686	2064
	BRACE3021517	109	218.. 523	2065
	BRACE3021805	110	312.. 1283	2066
	BRACE3022051	111	1042.. 1515	2067
10	BRACE3022303	112	2107.. 3009	2068
	BRACE3022312	113	98.. 1003	2069
	BRACE3022340	114	20.. 2785	2070
	BRACE3022847	115	560.. 1066	2071
	BRACE3023604	116	600.. >1057	2072
15	BRACE3024379	117	412.. 717	2073
	BRACE3024444	118	129.. 455	2074
	BRACE3024497	119	219.. 545	2075
	BRACE3024537	120	377.. 724	2076
	BRACE3024879	121	142.. 786	2077
20	BRACE3025627	122	1648.. 2019	2078
	BRACE3025719	123	111.. 1811	2079
	BRACE3026161	124	330.. 722	2080
	BRACE3026290	125	211.. 3225	2081
	BRACE3026345	126	2603.. 3145	2082
25	BRACE3026456	127	2113.. 2439	2083
	BRACE3026802	128	298.. 1260	2084
	BRACE3026844	129	1231.. 3081	2085
	BRACE3026947	130	1528.. 3849	2086
	BRACE3027256	131	670.. 1020	2087
30	BRACE3027931	132	64.. 1260	2088
	BRACE3028360	133	4486.. 4920	2089
	BRACE3028895	134	716.. 1129	2090
	BRACE3028998	135	264.. 785	2091
	BRACE3029005	136	394.. 771	2092
35	BRACE3029021	137	208.. 657	2093
	BRACE3029205	138	3800.. 4531	2094

	BRACE3029447	139	1873. . 2424	2095
	BRACE3030538	140	253. . 828	2096
	BRACE3031161	141	138. . 494	2097
	BRACE3031184	142	57. . 422	2098
5	BRACE3031185	143	11. . 370	2099
	BRACE3031315	144	1220. . 2563	2100
	BRACE3031372	145	1587. . 2429	2101
	BRACE3031579	146	1636. . 2079	2102
	BRACE3031728	147	22. . 2196	2103
10	BRACE3031743	148	53. . 805	2104
	BRACE3031843	149	115. . 429	2105
	BRACE3032385	150	103. . 2007	2106
	BRACE3032537	151	639. . 1199	2107
	BRACE3032538	152	3317. . 4198	2108
15	BRACE3032631	153	790. . 1701	2109
	BRACE3032980	154	223. . 618	2110
	BRACE3033525	155	1346. . 1672	2111
	BRACE3034183	156	190. . 1686	2112
	BRACE3034389	157	176. . 1294	2113
20	BRACE3034964	158	2385. . 3278	2114
	BRACE3034993	159	1533. . 1838	2115
	BRACE3035168	160	829. . 1149	2116
	BRACE3036156	161	3. . 338	2117
	BRACE3036271	162	2019. . 3125	2118
25	BRACE3036283	163	2599. . 3186	2119
	BRACE3037612	164	2401. . 2892	2120
	BRACE3037637	165	199. . 570	2121
	BRACE3037803	166	2507. . 2884	2122
	BRACE3038012	167	2134. . 2634	2123
30	BRACE3038030	168	976. . 1302	2124
	BRACE3038570	169	223. . 621	2125
	BRACE3038760	170	2145. . 2906	2126
	BRACE3039288	171	876. . 1511	2127
	BRACE3039358	172	385. . 2664	2128
35	BRACE3039378	173	479. . 2254	2129
	BRACE3039454	174	351. . 1073	2130

	BRACE3040012	175	145.. 465	2131
	BRACE3040239	176	1505.. 2548	2132
	BRACE3040504	177	307.. 738	2133
	BRACE3040644	178	1280.. 3214	2134
5	BRACE3040863	179	12.. 626	2135
	BRACE3041059	180	99.. 2558	2136
	BRACE3041162	181	2041.. 2604	2137
	BRACE3041827	182	3169.. 3561	2138
	BRACE3042046	183	1488.. 2879	2139
10	BRACE3042210	184	174.. 533	2140
	BRACE3042326	185	216.. 2366	2141
	BRACE3042409	186	238.. 3258	2142
	BRACE3042432	187	2084.. 2473	2143
	BRACE3042594	188	179.. 517	2144
15	BRACE3043597	189	23.. 460	2145
	BRACE3044090	190	1198.. 1602	2146
	BRACE3044172	191	803.. 3067	2147
	BRACE3044247	192	107.. 451	2148
	BRACE3044377	193	223.. 900	2149
20	BRACE3044495	194	893.. 1510	2150
	BRACE3045078	195	90.. 593	2151
	BRACE3045145	196	187.. 501	2152
	BRACE3045424	197	275.. 619	2153
	BRACE3045708	198	219.. 587	2154
25	BRACE3045981	199	302.. 724	2155
	BRACE3046049	200	849.. 1298	2156
	BRACE3046152	201	2241.. 3440	2157
	BRACE3046294	202	189.. 578	2158
	BRACE3046466	203	111.. 2969	2159
30	BRACE3046491	204	26.. 2275	2160
	BRACE3046609	205	1563.. 2477	2161
	BRACE3046837	206	25.. 558	2162
	BRACE3046855	207	3735.. 4247	2163
	BRACE3046966	208	12.. 452	2164
35	BRACE3047018	209	2886.. 3425	2165
	BRACE3047482	210	43.. 2313	2166

	BRACE3047801	211	17.. 3757	2167
	BRACE3048483	212	2340.. 2672	2168
	BRACE3048565	213	264.. 626	2169
	BRACE3048615	214	352.. 729	2170
5	BRACE3048677	215	238.. 732	2171
	BRACE3048756	216	2483.. 3052	2172
	BRACE3048904	217	229.. 759	2173
	BRACE3048905	218	1733.. 2038	2174
	BRACE3049186	219	106.. 519	2175
10	BRACE3049714	220	294.. 2957	2176
	BRACE3050270	221	2725.. 3291	2177
	BRACE3050504	222	287.. 1306	2178
	BRACE3051144	223	176.. 763	2179
	BRACE3051621	224	1748.. 3418	2180
15	BRACE3051627	225	1216.. 2235	2181
	BRACE3051722	226	816.. 1190	2182
	BRACE3051819	227	3.. 2801	2183
	BRACE3051879	228	193.. 519	2184
	BRACE3052321	229	124.. 1614	2185
20	BRACE3052410	230	17.. 2926	2186
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	TUTER2001433	1890	80..1579	3846
25	UTERU2000300	1891	608..1351	3847
	UTERU2014998	1892	876..1379	3848
	UTERU2016464	1893	662..1540	3849
	UTERU2016669	1894	111..758	3850
	UTERU2020226	1895	1256..1747	3851
30	UTERU2022955	1896	139..543	3852
	UTERU2023941	1897	121..687	3853
	UTERU2024042	1898	192..632	3854
	UTERU2027369	1899	161..697	3855
	UTERU2028377	1900	348..773	3856
35	UTERU2029660	1901	1766..2335	3857
	UTERU2035926	1902	187..552	3858

	UTERU2037423	1903	1228..2184	3859
	UTERU3000670	1904	122..5446	3860
	UTERU3001029	1905	1074..3416	3861
	UTERU3001394	1906	76..651	3862
5	UTERU3001946	1907	133..2736	3863
	UTERU3004635	1908	3..>5144	3864
	UTERU3005264	1909	2519..4000	3865
	UTERU3005422	1910	51..962	3866
	UTERU3006538	1911	2549..3055	3867
10	UTERU3006720	1912	1643..2821	3868
	UTERU3007108	1913	343..783	3869
	UTERU3009775	1914	1679..2092	3870
	UTERU3010029	1915	1769..2287	3871
	UTERU3010409	1916	2375..2902	3872
15	UTERU3010604	1917	243..761	3873
	UTERU3010892	1918	2018..2425	3874
	UTERU3010919	1919	125..1669	3875
	UTERU3011092	1920	1978..2853	3876
	UTERU3011398	1921	4299..4982	3877
20	UTERU3011558	1922	1239..3335	3878
	UTERU3011579	1923	160..795	3879
	UTERU3011837	1924	836..1627	3880
	UTERU3012293	1925	638..2485	3881
	UTERU3012414	1926	469..1170	3882
25	UTERU3012476	1927	66..425	3883
	UTERU3012599	1928	207..632	3884
	UTERU3012999	1929	1..501	3885
	UTERU3013167	1930	2919..3398	3886
	UTERU3013302	1931	1461..3221	3887
30	UTERU3014274	1932	58..540	3888
	UTERU3014647	1933	199..558	3889
	UTERU3014906	1934	5..625	3890
	UTERU3015011	1935	1055..2266	3891
	UTERU3015299	1936	470..937	3892
35	UTERU3015647	1937	771..1136	3893
	UTERU3015844	1938	1871..2188	3894

	UTERU3016070	1939	138. . 1613	3895
	UTERU3016273	1940	135. . 776	3896
	UTERU3016274	1941	226. . 1458	3897
	UTERU3016308	1942	220. . 1974	3898
5	UTERU3017441	1943	616. . 3621	3899
	UTERU3017626	1944	2588. . 3340	3900
	UTERU3017995	1945	1796. . 2227	3901
	UTERU3018172	1946	2006. . 2551	3902
	UTERU3018255	1947	259. . 741	3903
10	UTERU3019708	1948	993. . 2114	3904
	UTERU3020090	1949	1828. . 3153	3905
	UTERU3021231	1950	172. . 576	3906
	UTERU3021850	1951	665. . 1906	3907
	UTERU3022168	1952	61. . 3237	3908
15	UTERU3022588	1953	269. . 1717	3909
	UTERU3022922	1954	66. . 368	3910
	UTERU3023141	1955	93. . 947	3911
	UTERU3023413	1956	164. . 490	3912
	ADRGL2011190	3913	56. . 2113	3952
20	BRACE3002184	3914	199. . 1890	3953
	BRACE3026993	3915	143. . 4903	3954
	BRACE3046450	3916	361. . 4356	3955
	BRAMY3008096	3917	602. . 1396	3956
	BRAMY3016953	3918	4547. . 5188	3957
25	BRAWH3013197	3919	233. . 2623	3958
	BRAWH3028645	3920	256. . 1938	3959
	BRAWH3046240	3921	2257. . 3441	3960
	BRCAN2019772	3922	5. . 1273	3961
	BRHIP3030064	3923	3039. . 3347	3962
30	BRHIP3038037	3924	122. . 739	3963
	BRTHA3004432	3925	1988. . 2629	3964
	BRTHA3024233	3926	1440. . 2039	3965
	CTONG2002832	3927	346. . 2148	3966
	CTONG2003764	3928	1438. . 2169	3967
35	PLACE7013963	3929	2326. . >5202	3968
	PROST2010326	3930	298. . 1869	3969

	TBAES2004105	3931	135..>1864	3970
	TBAES2007379	3932	70..2118	3971
	TBAES2007481	3933	53..1162	3972
	TBAES2008133	3934	389..2719	3973
5	TEST12043585	3935	310..1296	3974
	TEST12046536	3936	111.. 533	3975
	TEST14002988	3937	597..2687	3976
	TEST14005158	3938	952..2961	3977
	TEST14005500	3939	249..2336	3978
10	TEST14052089	3940	1517..2038	3979
	THYMU3024602	3941	31..2634	3980
	THYMU3044175	3942	1101..2054	3981
	THYMU3046350	3943	282..1787	3982
	TLIVE2007192	3944	350.. 730	3983
15	TRACH1000193	3945	998..2956	3984
	TRACH3019290	3946	152..1738	3985
	TRACH3021066	3947	2485..3792	3986
	UTERU2017492	3948	80.. 808	3987
	UTERU2025415	3949	47.. 379	3988
20	UTERU2036507	3950	276..1691	3989
	UTERU3020583	3951	126.. 575	3990

Primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention, shown in SEQ ID NOs in Table 1 above. When synthesizing full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primer is usually 15-100 bp, and favorably between 15-35 bp. In the case of LA PCR, described below, a primer length of 25-35 bp provides a good result.

Methods for designing a primer that enables specific amplification based on a target nucleotide sequence are known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In principle, primers based on 5'-end sequences are designed such that amplification products will include the translation

start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of the 5' untranslated region (5'UTR), any part of the 5'-end, which ensures specificity to the cDNA of interest, can be selected as the primer.

When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. Such long nucleotides can be amplified using methods such as LA PCR (Long and Accurate PCR). The use of LA PCR is advantageous when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' → 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, amplification of nucleotides 20 kb or longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

Template DNAs for synthesizing the full-length cDNAs of the present invention can be obtained by using cDNA libraries prepared by various methods. The full-length cDNA clones of the present invention are clones with a high probability of completeness in length, obtained by a method comprising the steps of [1] preparing libraries containing cDNAs with a very high fullness ratio using oligo-capping, and [2] assembling 5'-end sequences and selecting those with the highest probability of completeness in length in clusters formed (there are many clones longer in the 5'-end direction).

However, the use of primers designed based on the full-length nucleotide sequences provided by the present invention enable full-length cDNAs to be easily obtained without using such a special technique.

The problem with commercially available cDNA libraries or those prepared by known methods is that mRNA contained in these libraries has a very low fullness ratio. Thus, it is difficult to screen full-length cDNA clones directly from the library using ordinary cloning methods. The present invention has

revealed nucleotide sequences of novel full-length cDNA. If such a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to more reliably synthesize a full-length cDNA.

The present invention provides isolated polynucleotides comprising the nucleotide sequences of SEQ ID NO: 1 as shown in Table 1, or homologs thereof. As used herein, an "isolated polynucleotide" is a polynucleotide whose structure is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which comprises the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in DNA libraries such as cDNA or genomic DNA libraries.

The 5'-end sequence of the full-length cDNA clones of this invention can be used to isolate the regulatory elements of transcription, including the promoter on the genome. A rough draft of the human genome (an analysis of the human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence will be

finished. However, using software to analyze transcription start sites on the human genome, in which long introns exist, is difficult. In contrast, it is easy to specify transcription start sites in the genomic sequence using nucleotide sequences which include the 5'-end of the full-length cDNA clones of the present invention, and thus it is easy to obtain genomic regions involved in transcription regulation, which include promoters contained upstream of the transcription start site.

The polypeptides encoded by the full-length cDNAs of the invention can be prepared as recombinant polypeptides or as natural polypeptides. For example, a recombinant polypeptide can be prepared by inserting a polynucleotide encoding a polypeptide of the present invention into a vector, introducing the vector into an appropriate host cell, and purifying the polypeptide expressed within that transformed host cell, as described below. In contrast, a natural polypeptide can be prepared, for example, by utilizing an affinity column to which is attached an antibody against a polypeptide of the present invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19). The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (see, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing a polypeptide of the invention.

The present invention provides substantially pure proteins encoded by the full-length cDNAs of the present invention. The term "substantially pure" herein used in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any appropriate standard method known in the art,

for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities of the polypeptides of the present invention, clarified in the above-mentioned manner. Whether or not a particular polypeptide is functionally equivalent to a polypeptide of the present invention can be verified by using the biological activity of the polypeptide of the present invention as an index to examine whether that polypeptide has the said activity.

Polypeptides functionally equivalent to polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into a polypeptide amino acid sequence (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5)). Such polypeptides can also be generated by spontaneous mutations. The present invention also includes polypeptides comprising the amino acid sequences shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have a function equivalent to that of a polypeptide identified in the Examples of the present invention, described later.

There are no limitations as to the number and site of amino acid mutation, as long as polypeptide function is maintained. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, five amino acids, preferably four or three amino acids, more preferably two amino acids, and further preferably one amino acid.

Herein "conservative amino acid substitution" refers to substitution of an amino acid residue belonging to a group

comprising a chemically similar side chain, with another amino acid in the same group. Groups of amino acid residues having similar side chains have been defined in the art. These groups include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using hybridization (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to a polynucleotide encoding the polypeptide identified in the present Example, based on the identified nucleotide sequence (Table 1) or a portion thereof, and obtain a functionally equivalent polypeptide from the isolated polynucleotide. The present invention includes polypeptides encoded by polynucleotides which hybridize with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to those identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated include but are not limited to vertebrates such as humans, mice, rats, rabbits, pigs and cows..

Washing conditions for hybridization for polynucleotide isolation encoding functionally equivalent polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following

conditions can be given as hybridization conditions of the present invention. Namely, conditions in which hybridization is performed at "6x SSC, 40% Formamide, 25°C", and washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which hybridization is performed at "6x SSC, 40% Formamide, 37°C", and washing at "0.2x SSC, 55°C". Even more preferable are those in which hybridization is performed at "6x SSC, 50% Formamide, 37°C", and washing at "0.1x SSC, 62°C". The more stringent the hybridization conditions, the more frequently polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and washing at "0.2x SSC, 55°C".

One skilled in the art can suitably select various conditions, such as SSC dilution ratio, formamide concentration, and temperature, to accomplish a similar stringency.

The above-mentioned combinations of SSC, SDS, and temperature conditions are indicated just as examples. Those skilled in the art can select hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors that determine hybridization stringency (for example, probe concentration, probe length, and duration of hybridization reaction).

The amino acid sequences of polypeptides isolated by using hybridization techniques usually have high identity to those of the polypeptides of the present invention, shown in Table 1. The present invention encompasses polynucleotides comprising a nucleotide sequence with high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses peptides, or polypeptides comprising an amino acid sequence with high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Even more

preferable is identity of 90% or more, 93% or more, or 95% or more. Further more preferable is 97% or more, or 99% or more. Identity can be determined using the BLAST search algorithm.

As used herein, "percent identity" of amino acid sequences
5 or nucleic acids is determined using the BLAST algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN
10 program, using for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, using for example, score = 50, wordlength = 3. When utilizing the BLAST and Gapped BLAST programs, the default parameters of each program are used. See <http://www.ncbi.nlm.nih.gov>.

15 Using the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4)) and primers designed based on the nucleotide sequences (Table 1) or portions thereof as identified in the present Example, it is possible to isolate
20 polynucleotide fragments highly homologous to the polynucleotide sequences or portions thereof, and to obtain polypeptides functionally equivalent to a particular polypeptide identified in the present Example, based on the isolated polynucleotide fragment.

25 The present invention also provides polynucleotides containing at least 15 nucleotides complementary to a polynucleotide comprising a nucleotide sequence of SEQ ID NOS shown in Table 1, or the complementary strand thereof. Herein, the term "complementary strand" is defined as the other strand
30 to one strand of a double stranded DNA composed of A:T and G:C base pairs. In addition, "complementary" is not only defined as sequences completely matching a continuous region of at least 15 nucleotides, but is also defined to include sequences comprising identity of at least 70%, favorably 80% or higher, more
35 favorably 90% or higher, and most favorably 95% or higher within

that region. Identity may be determined using the algorithm described herein.

Such polynucleotides includes probes and primers used for the detection and amplification of polynucleotides encoding the inventive polypeptides. When used as a primer, such a polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, such a polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the present invention, and comprises at least 15 bp. When used as a primer, such a polynucleotide is complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

Furthermore, polynucleotides of the present invention include antisense polynucleotides for suppressing the expression of a polypeptide of the present invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, using the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotides encoding a polypeptide of this invention (for example, the nucleotide sequences of SEQ ID NOs: 1 to 1956 and SEQ ID NOs: 3913 to 3951).

The present invention also includes polynucleotides that can use ribozyme or RNA interference (RNAi) activity to downregulate expression of a polynucleotide of the present invention, where such a polynucleotide can be designed based on the nucleotide sequence of the polynucleotide of the present invention.

A ribozyme is a polynucleotide that comprises 1) an antisense sequence of a polynucleotide of the present invention, and 2) the nucleotide sequence of a catalytic unit required for catalytic action. The antisense sequence constituting the
5 ribozyme can be appropriately selected to be compatible with the structure of the ribozyme's catalytic unit. The ribozyme's catalytic unit is well known in the art. For example, the hammer-head ribozyme (Rossi et al. (1991) Pharmac. Ther. 50: 245-254) and hairpin ribozyme (Hampel et al. (1990) Nucl. Acids
10 Res. 18: 299-304, and U.S. Pat. No. 5,254,678) are known to have nucleotide sequence-specific cleaving activity. These ribozymes use this catalytic activity to cleave, at a specific position, polynucleotides which hybridize to the antisense sequence.

For example, the autolytic domain of a hammer-head ribozyme
15 cleaves on the 3' side of C15 in the sequence G13U14C15. Base pairing between U14 and A9 plays an important role in this activity, and A15 or U15 can be cleaved instead of C15 (Koizumi M, et al: FEBS Lett 228: 228, 1988). A restriction enzyme-like RNA-cleaving ribozyme that recognizes the target RNA sequences
20 UC, UU, or UA can be produced by designing the ribozyme such that the substrate binding site complements the RNA sequence near the target site (Koizumi, M. et al., FEBS Lett, 239:285, 1988; Koizumi, M. and Otsuka, E., Protein, Nucleic acid, and Enzyme, 35:2191, 1990; Koizumi, M. et al., Nucl Acids Res,
25 17:7059, 1989). For example, the polynucleotides of the present invention (SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951) contain a number of potential target sites. The polynucleotides of the present invention can be cleaved at desired positions with a ribozyme which contains an appropriately selected antisense
30 sequence.

The ribozyme preferably comprises RNA and may be synthesized chemically or produced by enzymatic reaction. Methods of chemical synthesizing RNA are known in the art. Alternatively, the ribozyme can be produced by using RNA
35 polymerase to transcribe a polynucleotide encoding the ribozyme. To produce a ribozyme by transcription, a polynucleotide

encoding the ribozyme is arranged downstream of a promotor recognized by an RNA polymerase. Such RNA polymerases include T7 RNA polymerase and SP6 RNA polymerase. Alternatively, a ribozyme can be expressed in a host cell by inserting a polynucleotide encoding the ribozyme into an appropriate vector, and then introducing the vector into a host cell. The vector contains a promotor that can direct the expression of the gene in the host cell.

The present invention also provides siRNA (small interfering RNA) that downregulates the expression of a polynucleotide of the present invention. siRNA is a technique for controlling gene expression that inhibits protein synthesis from an mRNA by using a double-stranded RNA which comprises the same nucleotide sequence as that mRNA (Fire et al. (1998) Nature 391: 806-811). The effect of downregulating gene expression using double-stranded RNA is called "the RNAi effect". siRNA has been reported to effectively control gene expression in mice (Zamore et al. (2000) Cell 101:25-33; Gura (2000) Nature 404: 804-808). Thus the introduction of such a double-stranded RNA into cells can result in selective downregulation of target gene expression.

There is no limitation as to the length of the siRNAs. The double-stranded RNAs introduced into cells are enzymatically digested inside these cells, starting from their original 3' end and forming fragments of 21 bp to 23 bp. The enzyme that digests the double-stranded RNA is called 'dicer'. The resulting double-stranded RNA fragments recognize and bind to target nucleotide sequences which comprise the same sequence. The nucleotide sequence is then cleaved by the activity of RNase III-like nuclease (Hammond et al. (2000) Nature, 404: 293-298; Zamore et al. (2000) Cell 101: 25-33).

siRNA is introduced into cells to downregulate gene expression using RNAi activity. siRNA can be introduced into cells using the same methods as for ribozymes. Specifically, chemically-synthesized, double-stranded RNA can be introduced into cells. When synthesized RNA, including antisense RNA and

siRNA, is intended for introduction into cells, it can be pre-modified to prevent degradation by nuclease. For example, thiolated RNA is protected from nuclease degradation.

Alternatively, siRNA can be expressed in cells. For
5 example, siRNA can be expressed in cells by inserting a sense sequence and its corresponding antisense sequence into a vector, and then transforming cells with that vector. When the two strands are adjacent, the expressed double-stranded RNA will have a hairpin-loop structure. When the two strands are
10 expressed under the control of different promoters, the resulting double-stranded RNA will comprise two separate strands. Promoters generally used for the expression of siRNA include the U6 promotor.

The nucleotide sequence of an antisense polynucleotide,
15 ribozyme, or siRNA of the present invention may be completely identical or complementary to any one of the nucleotide sequences of SEQ ID NOs: 1-1956 and SEQ ID NOs: 3913-3951, or may have high homology to these nucleotide sequences. The phrase "high homology" to an antisense polynucleotide, ribozyme,
20 or siRNA nucleotide sequence typically means 90% or higher homology, preferably 95% or higher homology, more preferably 98% or higher homology, and still more preferably 99% or higher homology. The homology of a nucleotide sequence can be estimated, for example, by a method described herein.

25 One skilled in the art can design siRNA based on the nucleotide sequence of a gene whose expression is to be downregulated. The typical methods for designing siRNA include, for example, those described below. To begin with, it is advantageous to avoid using as target sequences: 1) 5'- or 3'-
30 untranslated regions, and 2) regions adjacent to the start codon.

These regions often serve as binding regions for transcriptional regulatory proteins. In addition, these regions may also contain nucleotide sequences conserved among various mRNAs, and thus they may act to inhibit the expression of genes
35 other than the gene of interest.

Thus, it may be advantageous to arrange the target sequence, for example, within the ORF downstream of the start codon. It is preferable to adjust the number of nucleotides between the start codon and the target sequence, for example, to 50
5 nucleotides or more. Typically, the nucleotide sequence of an siRNA is designed so that it starts from an aa sequence and comprises 19-21 consecutive nucleotides. A dinucleotide overhang is added to one end of siRNA. The nucleotide sequence of such an overhang may include doublets, dTdT or UU sequences.
10 The GC content of a nucleotide sequence constituting siRNA is preferably about 50%. G and C nucleotide residues are preferably uniformly distributed throughout the siRNA.

The action of siRNA is based on sequence-specific mRNA hybridization. Thus, to achieve downregulation specific to a
15 particular gene, it is essential to make the target nucleotide sequence as specific as possible to that gene. It is thus preferable to use homology searches to confirm that the proposed target nucleotide sequence exhibits negligible homology with other genes. Nucleotide sequence homology can be determined
20 using established algorithms.

As long as an siRNA of the present invention downregulates the expression of a polynucleotide of the present invention, it is not limited to nucleotide sequences obtained using the typical design method described above. For example, even if the
25 target sequence is not specific to the nucleotide sequence of a particular gene, it can specifically downregulate the expression of a gene of interest in cells which do not express genes comprising homologous nucleotide sequences. Furthermore, double-stranded RNA having RNAi activity can be obtained without
30 using the above-described methods typically used to select a target sequence.

The polynucleotides or antisense polynucleotides, ribozymes, and siRNAs of the present invention can be used in, for example, gene therapy. Preferable target diseases may be, for example,
35 cancers or various inflammatory diseases. Such molecules can be used for gene therapy, for example, by administering them to

patients *in vivo* or *ex vivo* using viral vectors such as retroviral vectors, adenoviral vectors, and adeno-related viral vectors, or non-viral vectors such as liposomes.

5 The present invention also includes partial peptides of the polypeptides of the invention. Such a partial peptide comprises a polypeptide generated as a result of removing a signal peptide from a secretory protein. If a polypeptide of the present invention has activity as a receptor or ligand, the partial peptide may function as a competitive inhibitor of the
10 polypeptide, and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific to a polypeptide of the present invention, the peptides comprise at least seven amino acids, preferably eight amino acids or more,
15 more preferably nine amino acids or more, and even more preferably ten amino acids or more. The peptide can be used to prepare an antibody against or competitive inhibitor of a polypeptide of the present invention, and can also be used to screen for a receptor that binds to the polypeptide of this
20 invention. The partial peptides of this invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or by digesting a polypeptide of the invention with an appropriate peptidase.

The present invention also relates to a vector into which a
25 polynucleotide of the invention is inserted. Vectors of the present invention are not limited as long as they can contain the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferred cloning vectors. To produce a polypeptide of the
30 invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for
35 *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8:

466-472) for *in vivo* expression. To insert a polynucleotide of the present invention, ligation utilizing restriction sites can be performed according to standard methods (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

The GATEWAYTM system (Invitrogen), which is an expression vector construction system for polypeptide expression, can also be used (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASETM and LR CLONASETM) derived from lambda phage and uses BP CLONASETM-specific recombination sites for the Entry Vector, and LR CLONASETM-specific recombination sites for the Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, a second recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and efficiently. Using the above-mentioned typical restriction enzyme/ligase reaction method, expression vector construction and expression of a polypeptide of interest takes about seven to ten days. However, using the GATEWAYTM system, the polypeptide of interest can be expressed and prepared in only three to four days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (<http://biotech.nikkeibp.co.jp/netlink/lto/gateway/>).

The present invention also relates to a transformant carrying a vector of the present invention. Any cell can be used as a host into which a vector of this invention is inserted, and various kinds of host cells can be used depending on the purpose. For example, COS cells or CHO cells can be used for strong expression of the polypeptide in eukaryotic cells.

Introduction of such a vector into host cells can be performed, for example, by calcium phosphate precipitation, electroporation (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9),
5 lipofectamine method (GIBCO-BRL), or microinjection, etc.

Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1, or the complementary strand thereof, can
10 be used not only as a primer for synthesizing full-length cDNAs, but also for testing and diagnosing abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using a polynucleotide of this
15 invention as a primer, a polynucleotide encoding a polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization, since the transcription start site within the genomic sequence can be easily specified based on the
20 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of sequence abnormality using RFLP analysis, SSCP, or sequencing. Where expression of an mRNA of the present invention varies according to a specific disease, analysis of the amount of mRNA expression
25 using a polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of that disease.

The present invention also relates to antibodies that bind to a polypeptide of the present invention. There are no limitations as to the form of the antibodies of this invention.
30 They include polyclonal antibodies, monoclonal antibodies, or portions thereof that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

35 A polyclonal antibody of this invention can be obtained according to the standard method of synthesizing an oligopeptide

corresponding to an amino acid sequence, and immunizing rabbits with that peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). A monoclonal antibody of the present invention can be obtained according to the standard method of purifying a polypeptide expressed in *E. coli*, immunizing mice with that polypeptide, and producing a hybridoma cell by fusing spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

An antibody binding to a polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of abnormalities of the expression and structure of that polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and a polypeptide of this invention can then be detected for the above purpose using Western blotting, immunoprecipitation, or ELISA.

Furthermore, an antibody binding to a polypeptide of the present invention can be utilized for treating a disease associated with that polypeptide. If the antibody is used to treat patients, human antibodies, humanized antibodies, or chimeric antibodies are preferred due to their low antigenicity. Human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of a human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). These humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

The cDNAs (clones) of the present invention include polypeptide sequences encoding proteins whose function can be predicted, such as, for example, secretory and/or membrane proteins, glycoprotein-related proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, enzyme and/or metabolism-related proteins, cell division- and/or cell proliferation-related proteins,

cytoskeleton-related proteins, nuclear protein and/or RNA synthesis-related proteins, protein synthesis and/or transport-related proteins, cellular defense-related proteins, development and/or differentiation-related proteins, DNA- and/or RNA-binding proteins, ATP- and/or GTP-binding proteins. The results of cDNA
5 homology searches can be used to estimate whether a cDNA sequence comprises the function of an above-described protein. Specifically, the function of a polypeptide encoded by a cDNA of the present invention can be inferred by (a) searching for a
10 known gene or protein which is homologous to the complete or partial nucleotide sequence of the full-length cDNA of the present invention, and (b) comparing the function of the gene and that of the protein encoded by the gene.

Alternatively, the function of a polypeptide encoded by a
15 cDNA of the present invention can be predicted when a signal sequence, transmembrane domain, nuclear translocation signal, glycosylation signal, phosphorylation site, zinc-finger motif, SH3 domain, or such is found in the amino acid sequence. In particular, partial sequence structures such as motif and domain
20 structures are commonly found in a number of proteins, and comprise a minimal functional protein structure. The Pfam database identifies a total of 4,832 types of motifs and domains, including both those whose functions have been clarified and those whose functions remain unclear
25 (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) Version 7.7 (the latest version as of December 2002).

A specific example of motif/domain function is shown below. The ITAM motif (immunoreceptor tyrosine-based activation motif) is found in the intracellular region of the T cell receptor
30 which is expressed on the cell membrane of T cells participating in an immune response (Flaswinkel, H. et al. Semin Immunol 1995 Feb,7(1):21-7). The ITAM motif has a tandem YXXL structure (tyrosine-arbitrary amino acid-arbitrary amino acid-leucine). On extracellular stimulus by an antigen or antibody, the
35 tyrosine in the motif is phosphorylated by an enzyme (LCK) with a kinase domain. Then, ZAP70 binds to the phosphorylated

tyrosine via the SH2 domain, resulting in downstream signal transduction (Bu, J.Y. et al., Proc Natl Acad Sci U S A 1995 May 23, 92(11):5106-10; Neumeister, E.N. et al., Mol Cell Biol 1995 June, 15(6):3171-8).

5 A similar phenomenon has been found in mast cells as well as in T cells (Chen, T. et al., J Biol Chem 1996 Oct 11, 271(41):25308-15). Thus, at the molecular level, such a phenomenon is the first step in the activation of immune cells in immunologic diseases such as allergies, atopic dermatitis,
10 and asthma.

 Even in a simple exemplary scheme such as the one described above, there are three major motif/domain structures - ITAM, the SH2 domain, and the protein kinase domain - each of which play an important role. The mechanism of this scheme can be
15 interpreted using these three structures. Thus, collecting, categorizing and elucidating the function of molecules that comprise common motif/domain structures is exceedingly important in understanding the molecular-based mechanisms of various cellular functions, including and in addition to the immune
20 response described herein. Searching for motif/domain structures is highly important as the first step in elucidating the functions of unknown polypeptides. It is also understood that an entire polypeptide structure is comprised by minimal structures such as motifs and domains, thus providing the
25 overall function of an entire polypeptide.

 The overall function of a polypeptide in cells can be accurately predicted at the molecular level using data obtained by domain and motif structure analysis. In addition, a fusion polypeptide comprising a partial amino acid sequence and a GFP
30 protein or the like may be prepared, and then introduced into cultured cells. For example, if a polypeptide is localized on the cell membrane, it may function as a receptor or ion channel. Alternatively, if a polypeptide is localized in the nucleus, it can be predicted to serve as a polynucleotide-binding protein or
35 to participate in transcription. Thus, the function of a

polypeptide can also be predicted by determining its localization.

The function of a full-length cDNA obtained in the present invention can be predicted by carrying out the above-described analysis using its entire nucleotide sequence and the amino acid sequence it encodes. Even when the full-length cDNA nucleotide sequence is not available, however, a partial sequence thereof (preferably 300 nucleotides or more) often enables function to be predicted. However, function predicted based on information yielded in a partial sequence homology search will not necessarily be the same as that based on a full-length sequence. Functional prediction based on a full-length nucleotide sequence is obviously preferable.

A more specific method for predicting function involves homology searches of databases such as GenBank, Swiss-Prot, UniGene, nr and RefSeq, using BLAST or FASTA. The functions of polypeptides encoded by the cDNAs of the present invention can be predicted based on hit genes and the function of polypeptides encoded by these genes. Polypeptide functions can be predicted from the amino acid sequences deduced from the structure of the full-length nucleotide sequences. In this way, signal sequences and transmembrane domains can be predicted from amino acid sequences using PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14, 378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.), MEMSAT [D. T. Jones, W. R. Taylor & J. M. Thornton, Biochemistry, 33, 3038-3049 (1994)], and the like. Alternatively, motifs and domains can be predicted from amino acid sequences by carrying out searches using Pfam, PROSITE (<http://www.expasy.ch/prosite/>), or such. The above-described procedures facilitate more accurate prediction of polypeptide function.

The databases GenBank, Swiss-Prot, nr and RefSeq were searched as described above for homology to the 1,995 full-length clone sequences of the present invention whose full-length nucleotide had been determined (see Example 4 and the results of homology searches). In addition, the amino acid

sequences deduced from the full-length nucleotide sequences were analyzed by database searches for signal sequences and transmembrane domains using PSORT and SOSUI (see Example 5). The clones were categorized into the fourteen functional categories shown below, based on 1) the results of annotation-based functional prediction (by referring to keywords in the hit data of Swiss-Prot, or to Definitions and Reference information in the hit data of nr or RefSeq), 2) the results of PSORT searches for signal sequences using the deduced ORFs and 3) the results of SOSUI searches for transmembrane domains using the deduced ORFs. As a result, 1,006 clones were estimated to encode proteins belonging to the categories described below.

- Secretory and/or membrane protein (570 clones)
- Glycoprotein-related protein (124 clones)
- 15 Signal transduction-related protein (75 clones)
- Transcription-related protein (113 clones)
- Disease-related protein (414 clones)
- Enzyme and/or metabolism-related protein (172 clones)
- Cell division- and/or cell proliferation-related protein (29 clones)
- 20 Cytoskeleton-related protein (61 clones)
- Nuclear protein and/or RNA synthesis-related protein (41 clones)
- Protein synthesis- and/or transport-related protein (52 clones)
- Cellular defense-related protein (five clones)
- 25 Development and/or differentiation-related protein (17 clones)
- DNA- and/or RNA-binding protein (127 clones)
- ATP- and/or GTP-binding protein (70 clones)

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 551 clones.

- 30 3NB692004045, ADIPS2000069, ADRGL2010315, ASTRO2015162, BLADE2001031, BLADE2002744, BLADE2007744, BRACE2003628, BRACE2012528, BRACE2013126, BRACE2017397, BRACE2017580, BRACE2017992, BRACE2023633, BRACE2030039, BRACE2035191, BRACE3001403, BRACE3001973, BRACE3002264, BRACE3002756,
- 35 BRACE3004767, BRACE3004981, BRACE3007869, BRACE3009392, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3015898,

BRACE3018083, BRACE3021517, BRACE3021805, BRACE3022051,
 BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024879,
 BRACE3026345, BRACE3026456, BRACE3026802, BRACE3028360,
 BRACE3029021, BRACE3030538, BRACE3031372, BRACE3031579,
 5 BRACE3031728, BRACE3032385, BRACE3032537, BRACE3032980,
 BRACE3033525, BRACE3034964, BRACE3034993, BRACE3037637,
 BRACE3037803, BRACE3038570, BRACE3039358, BRACE3039378,
 BRACE3040644, BRACE3040863, BRACE3042326, BRACE3042409,
 BRACE3042432, BRACE3044090, BRACE3046049, BRACE3046466,
 10 BRACE3048565, BRACE3050504, BRACE3051144, BRACE3051621,
 BRACE3052486, BRALZ2010842, BRALZ2011337, BRALZ2013690,
 BRAMY2015516, BRAMY2021098, BRAMY2025495, BRAMY2037609,
 BRAMY2041507, BRAMY2044686, BRAMY2046537, BRAMY3002886,
 BRAMY3004126, BRAMY3007449, BRAMY3009556, BRAMY3009904,
 15 BRAMY3010654, BRAMY3010902, BRAMY3015549, BRAMY3016829,
 BRAMY3018248, BRAWH2000256, BRAWH2010364, BRAWH2011812,
 BRAWH2011958, BRAWH2012866, BRAWH2014053, BRAWH2016209,
 BRAWH2016305, BRAWH3001053, BRAWH3001783, BRAWH3001833,
 BRAWH3003573, BRAWH3005892, BRAWH3008867, BRAWH3010461,
 20 BRAWH3010657, BRAWH3011907, BRAWH3012005, BRAWH3012662,
 BRAWH3012779, BRAWH3013049, BRAWH3014609, BRAWH3015175,
 BRAWH3016123, BRAWH3017259, BRAWH3018063, BRAWH3018548,
 BRAWH3018969, BRAWH3019529, BRAWH3019820, BRAWH3020200,
 BRAWH3020884, BRAWH3021012, BRAWH3021641, BRAWH3022347,
 25 BRAWH3023156, BRAWH3023274, BRAWH3023415, BRAWH3023421,
 BRAWH3024186, BRAWH3024242, BRAWH3027574, BRAWH3027880,
 BRAWH3028223, BRAWH3028754, BRAWH3029806, BRAWH3030810,
 BRAWH3032298, BRAWH3034114, BRAWH3034134, BRAWH3035914,
 BRAWH3036270, BRAWH3038055, BRAWH3038324, BRAWH3040711,
 30 BRAWH3040900, BRAWH3042132, BRAWH3042772, BRAWH3042996,
 BRAWH3043498, BRAWH3043623, BRAWH3044151, BRAWH3044676,
 BRAWH3046196, BRAWH3047063, BRAWH3048374, BRAWH3048724,
 BRAWH3049068, BRAWH3049544, BRCAN2002662, BRCAN2003269,
 BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2015402,
 35 BRCAN2018269, BRCAN2019653, BRCAN2019907, BRCAN2020234,
 BRCAN2020412, BRCAN2020972, BRCAN2021325, BRCAN2022126,

BRCOC2006164, BRCOC2006639, BRCOC2009638, BRHIP2006921,
 BRHIP2020930, BRHIP2021929, BRHIP3000859, BRHIP3001878,
 BRHIP3002000, BRHIP3002124, BRHIP3003063, BRHIP3003306,
 BRHIP3003395, BRHIP3004774, BRHIP3005801, BRHIP3005944,
 5 BRHIP3006950, BRHIP3007195, BRHIP3007424, BRHIP3007960,
 BRHIP3008320, BRHIP3010289, BRHIP3011269, BRHIP3011831,
 BRHIP3012185, BRHIP3012357, BRHIP3012997, BRHIP3013078,
 BRHIP3016032, BRHIP3017146, BRHIP3017558, BRHIP3019956,
 BRHIP3020733, BRHIP3021019, BRHIP3025795, BRHIP3025844,
 10 BRHIP3027160, BRHIP3027191, BRHIP3028742, BRHIP3029530,
 BRHIP3030230, BRHIP3031733, BRHIP3035222, BRHIP3035754,
 BRHIP3036715, BRHIP3036936, BRHIP3037810, BRHIP3039430,
 BRHIP3039509, BRSSN2004710, BRSSN2018218, BRSTN2010089,
 BRSTN2011688, BRSTN2011899, BRSTN2011961, BRTHA2000969,
 15 BRTHA2003759, BRTHA2012189, BRTHA2014647, BRTHA2018304,
 BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566,
 BRTHA2020721, BRTHA2020781, BRTHA2021212, BRTHA2021440,
 BRTHA2021450, BRTHA2022914, BRTHA2022968, BRTHA2023437,
 BRTHA2026311, BRTHA2027250, BRTHA2030036, BRTHA2031917,
 20 BRTHA2033155, BRTHA2033320, BRTHA2033469, BRTHA2033683,
 BRTHA2036055, BRTHA2036295, BRTHA3003225, BRTHA3006593,
 BRTHA3010135, BRTHA3010540, BRTHA3010717, BRTHA3011194,
 BRTHA3011998, BRTHA3012265, BRTHA3013882, BRTHA3014835,
 BRTHA3016616, BRTHA3018623, BRTHA3026161, BRTHA3027820,
 25 BRTHA3028505, CHONS2001287, CHONS2001797, CHONS2002419,
 COLON2004351, COLON2005623, COLON2005735, CTONG2008989,
 CTONG2020582, CTONG2027150, CTONG3001605, CTONG3002588,
 CTONG3008223, FCBBF3012443, FEBRA2023498, FEBRA2026977,
 FEHRT2002708, FEKID2002231, FEKID2002493, FELNG2000720,
 30 FELNG2001706, HCHON2009766, HSYRA2004550, JCMLC1000159,
 JCMLC2000273, JCMLC2002095, JCMLC2002751, KIDNE2004531,
 KIDNE2015987, KIDNE2017153, LYMPB1000158, LYMPB2002236,
 LYMPB2002458, LYMPB2002478, MESAN2014624, NETRP2004090,
 NETRP2004434, NETRP2005282, NETRP2005849, NETRP2008582,
 35 NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3009524,
 NT2RP7019682, NT2RP8001605, NT2RP8003787, NT2RP8008057,

OCBBF2000831, OCBBF2004478, OCBBF2007039, OCBBF2009536,
OCBBF2018229, OCBBF2018618, OCBBF2036019, OCBBF3003745,
OCBBF3007704, OCBBF3021502, OCBBF3022123, OCBBF3022576,
OCBBF3023175, OCBBF3023993, OCBBF3025475, OCBBF3025887,
5 OCBBF3026979, OCBBF3028001, PEBLM2003935, PEBLM2005615,
PLACE5000522, PLACE6000012, PLACE6010936, PLACE6019674,
PLACE7000266, PLACE7000707, PLACE7001759, PLACE7003639,
PLACE7006090, PLACE7006498, PLACE7008136, PLACE7011269,
PLACE7012111, PLACE7016321, PLACE7016454, PUAEN2000684,
10 SMINT2003641, SPLEN2011252, SPLEN2025012, SPLEN2031004,
SPLEN2034551, SPLEN2035615, SPLEN2042051, STOMA2004663,
SYNOV4009139, T1ESE2002665, TBAES2005361, TBAES2007428,
TESOP2008556, TESTI2003768, TESTI2007490, TESTI2018335,
TESTI2022323, TESTI2024267, TESTI2028613, TESTI2036822,
15 TESTI2037085, TESTI2037657, TESTI2037877, TESTI2046188,
TESTI2049041, TESTI2052670, TESTI4001037, TESTI4002072,
TESTI4002889, TESTI4003602, TESTI4004539, TESTI4004653,
TESTI4005399, TESTI4007671, TESTI4010544, TESTI4010721,
TESTI4013774, TESTI4014415, TESTI4014932, TESTI4014977,
20 TESTI4017647, TESTI4017854, TESTI4019149, TESTI4021197,
TESTI4021377, TESTI4021569, TESTI4022158, TESTI4023096,
TESTI4023654, TESTI4024494, TESTI4026680, TESTI4027170,
TESTI4028042, TESTI4031173, TESTI4031818, TESTI4032128,
TESTI4034973, TESTI4035872, TESTI4035989, TESTI4036012,
25 TESTI4037949, TESTI4038047, TESTI4040559, TESTI4041049,
TESTI4043067, TESTI4043371, TESTI4045168, TESTI4046450,
TESTI4047119, TESTI4048296, TESTI4048545, TESTI4051015,
TESTI4051858, TESTI4052219, TESTI4052430, TESTI4052598,
THYMU3002825, THYMU3003007, THYMU3003350, THYMU3008935,
30 THYMU3009755, THYMU3011360, THYMU3013197, THYMU3014173,
THYMU3015457, THYMU3015647, THYMU3016518, THYMU3018151,
THYMU3019605, THYMU3021404, THYMU3022211, THYMU3022528,
THYMU3022668, THYMU3023107, THYMU3023400, THYMU3025118,
THYMU3025313, THYMU3025642, THYMU3026306, THYMU3026532,
35 THYMU3026869, THYMU3027540, THYMU3028461, THYMU3029795,
THYMU3031878, THYMU3032032, THYMU3033649, THYMU3033754,

THYMU3034099, THYMU3034616, THYMU3036310, THYMU3036934,
 THYMU3036953, THYMU3037192, THYMU3037772, THYMU3038158,
 THYMU3038167, THYMU3040068, THYMU3040126, THYMU3040146,
 THYMU3040172, THYMU3040746, THYMU3040816, THYMU3041918,
 5 THYMU3042321, THYMU3043688, THYMU3043779, THYMU3044188,
 THYMU3045510, THYMU3047115, THYMU3047156, THYMU3047542,
 THYMU3047760, TKIDN2011160, TLIVE2008797, TRACH3003872,
 TRACH3004747, TRACH3005274, TRACH3005699, TRACH3007274,
 TRACH3007625, TRACH3009008, TRACH3009061, TRACH3010382,
 10 TRACH3011082, TRACH3011184, TRACH3012659, TRACH3012891,
 TRACH3013900, TRACH3014063, TRACH3014580, TRACH3015136,
 TRACH3015346, TRACH3016368, TRACH3016885, TRACH3016992,
 TRACH3017409, TRACH3018191, TRACH3018240, TRACH3018524,
 TRACH3018943, TRACH3019058, TRACH3019370, TRACH3019621,
 15 TRACH3019807, TRACH3020930, TRACH3021023, TRACH3021544,
 TRACH3022758, TRACH3023063, TRACH3023203, TRACH3023516,
 TRACH3023945, TRACH3024081, TRACH3024671, TRACH3025346,
 TRACH3026542, TRACH3027681, TRACH3029670, TRACH3031316,
 TRACH3031678, TRACH3032480, TRACH3034680, TRACH3036103,
 20 TRACH3036278, TSTOM2002682, UTERU3005422, UTERU3010029,
 UTERU3011092, UTERU3011398, UTERU3011837, UTERU3012414,
 UTERU3015647, UTERU3016273, UTERU3017626, UTERU3021850,
 UTERU3022168, UTERU3022922, UTERU3023413

The following 19 clones are also predicted to belong to the
 25 category of secretory protein and/or membrane protein.

ADRGL2011190, BRACE3046450, BRAWH3013197, BRAWH3028645,
 BRAWH3046240, BRTHA3024233, PROST2010326, TBAES2004105,
 TBAES2007379, TBAES2007481, TBAES2008133, TESTI2043585,
 TESTI4005158, THYMU3024602, THYMU3044175, THYMU3046350,
 30 TLIVE2007192, UTERU2025415, UTERU2036507

The clones predicted to belong to the category of
 glycoprotein-related protein are the following 114 clones.

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3001403,
 BRACE3001973, BRACE3002264, BRACE3009392, BRACE3026345,
 35 BRACE3032385, BRACE3039358, BRACE3039378, BRACE3042432,
 BRACE3046466, BRACE3051621, BRAMY3004126, BRAWH2012866,

BRAWH3001783, BRAWH3003573, BRAWH3014609, BRAWH3023156,
 BRAWH3024186, BRAWH3029806, BRAWH3040900, BRAWH3043623,
 BRAWH3044151, BRAWH3049544, BRCAN2003269, BRCAN2021325,
 BRHIP3005944, BRHIP3007424, BRHIP3010289, BRHIP3011269,
 5 BRHIP3011567, BRHIP3030230, BRHIP3036715, BRHIP3036936,
 BRHIP3039509, BRTHA2019726, BRTHA2020721, BRTHA2022968,
 BRTHA2025869, BRTHA2027250, BRTHA2031917, BRTHA2033155,
 BRTHA2033683, BRTHA3010135, CHONS2001287, COLON2004351,
 FEKID2002493, FELNG2000720, JCMLC1000159, JCMLC2000273,
 10 JCMLC2002095, JCMLC2002751, KIDNE2015987, LYMPB2002458,
 NT2RI3005923, NT2RI3009524, OCBBF2000831, OCBBF2004478,
 OCBBF2007039, OCBBF2018618, OCBBF3026979, PEBLM2005615,
 PLACE6001933, PLACE6010936, PLACE7006090, PLACE7012111,
 SPLEN2025012, STOMA2004663, T1ESE2002665, TESTI2007490,
 15 TESTI2022323, TESTI2037657, TESTI2052670, TESTI4001517,
 TESTI4014932, TESTI4031173, THYMU3014173, THYMU3015647,
 THYMU3016518, THYMU3020221, THYMU3025118, THYMU3026532,
 THYMU3032032, THYMU3037772, THYMU3040172, TKIDN2011160,
 TLUNG2001445, TRACH3005274, TRACH3009061, TRACH3015136,
 20 TRACH3018524, TRACH3018907, TRACH3019058, TRACH3019370,
 TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023,
 TRACH3023516, TRACH3025346, TRACH3026299, TRACH3028441,
 TRACH3029670, TRACH3031678, TRACH3034680, TRACH3037505,
 TRACH3038399, TUTER2001433, UTERU3011398, UTERU3011837,
 25 UTERU3015647, UTERU3021850

The following ten clones are also predicted to belong to the category of glycoprotein-related protein.

BRAWH3013197, BRAWH3046240, PROST2010326, TBAES2004105,
 TESTI2043585, TESTI4005158, THYMU3024602, THYMU3046350,
 30 TRACH3021066, UTERU2036507

The clones predicted to belong to the category of signal transduction-related protein are the following 71 clones.

BRACE3002344, BRACE3017253, BRACE3031315, BRACE3036283,
 BRACE3042046, BRACE3044172, BRACE3046491, BRACE3046609,
 35 BRAMY3009491, BRAMY3015547, BRAMY3017920, BRAWH3017180,
 BRAWH3019026, BRAWH3027806, BRAWH3032340, BRAWH3042438,

BRAWH3047644, BRCAN2010665, BRHIP3006294, BRHIP3011460,
 BRHIP3011567, BRHIP3033557, BRHIP3037543, BRHIP3041587,
 BRTHA2026290, BRTHA2035743, BRTHA3011187, BRTHA3021708,
 BRTHA3025073, BRTHA3026916, KIDNE2010049, N1ESE2000698,
 5 OCBBF3005330, OCBBF3006986, OCBBF3009244, OCBBF3025630,
 PLACE6000055, PLACE6001933, PLACE7009936, PLACE7011559,
 PLACE7014247, PUAEN2006639, SKMUS2008585, SPLEN2007689,
 TESTI2021654, TESTI2040377, TESTI4010902, TESTI4013474,
 TESTI4046073, TESTI4049786, TESTI4051865, THYMU3013785,
 10 THYMU3025683, THYMU3032798, TRACH3003037, TRACH3003357,
 TRACH3005173, TRACH3018519, TRACH3018606, TRACH3024020,
 TRACH3026650, TRACH3027701, TRACH3029462, TRACH3030176,
 TRACH3038399, TSTOM2001571, TSTOM2002611, UTERU2024042,
 UTERU3001029, UTERU3010919, UTERU3021231

15 The following four clones are also predicted to belong to
 the category of signal transduction-related protein.

BRHIP3030064, CTONG2003764, PLACE7013963, TRACH3021066

The clones predicted to belong to the category of
 transcription-related protein are the following 106 clones.

20 ASTRO2016114, BEAST2000981, BRACE2012947, BRACE2019348,
 BRACE3025719, BRACE3026844, BRACE3034183, BRACE3041162,
 BRACE3046152, BRAMY2040915, BRAMY3000692, BRAMY3007078,
 BRAMY3011581, BRAMY3014027, BRAMY3018754, BRAWH3000446,
 BRAWH3005886, BRAWH3011577, BRAWH3013009, BRAWH3013264,
 25 BRAWH3017477, BRAWH3023172, BRAWH3028796, BRAWH3031342,
 BRAWH3032571, BRAWH3035936, BRAWH3036247, BRAWH3036334,
 BRAWH3038827, BRCOC2012386, BRHIP2023735, BRHIP2027077,
 BRHIP2029529, BRHIP3004725, BRHIP3027651, BRHIP3028246,
 BRTHA2024712, BRTHA3000456, BRTHA3003736, BRTHA3010212,
 30 BRTHA3014000, BRTHA3028339, CHONS2000797, CHONS2002829,
 CTONG2001932, CTONG2011801, D9OST2003106, FCBBF3020030,
 FCBBF5000384, HCASM2008154, NETRP2004017, NT2RI3008179,
 NT2RI3009480, NT2RP8003490, NTONG2003805, NTONG2008483,
 OCBBF2016928, OCBBF3005330, OCBBF3008392, OCBBF3020263,
 35 OCBBF3021361, OCBBF3022166, PLACE7002303, PLACE7005169,
 PLACE7009757, SPLEN2012571, SPLEN2028417, SYNOV2003326,

T1ESE2000904, TESTI2040377, TESTI4001679, TESTI4002799,
 TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322,
 TESTI4005470, TESTI4039904, TESTI4052775, THYMU3008105,
 THYMU3012983, THYMU3014372, THYMU3020869, THYMU3021586,
 5 THYMU3022434, THYMU3026000, THYMU3030072, THYMU3037052,
 THYMU3043200, TLIVE2001616, TRACH3003037, TRACH3003458,
 TRACH3004424, TRACH3010079, TRACH3010167, TRACH3010342,
 TRACH3015951, TRACH3021883, TRACH3022109, TRACH3028180,
 TRACH3036750, UTERU2037423, UTERU3012293, UTERU3016070,
 10 UTERU3019708, UTERU3022588

The following seven clones are also predicted to belong to the category of transcription-related protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI4002988,
 TESTI4005500, TRACH1000193, TRACH3019290

15 The clones predicted to belong to the category of disease-related protein are the following 391 clones.

ADIPS2000069, ASTRO2015162, ASTRO2016114, ASTRO3000154,
 BLADE2000256, BRACE1000475, BRACE2012838, BRACE2012947,
 BRACE2013009, BRACE2016896, BRACE2017397, BRACE2023744,
 20 BRACE2027382, BRACE3001403, BRACE3001973, BRACE3002756,
 BRACE3004767, BRACE3009392, BRACE3013418, BRACE3018083,
 BRACE3019941, BRACE3020669, BRACE3025719, BRACE3026345,
 BRACE3026802, BRACE3028998, BRACE3036283, BRACE3039378,
 BRACE3040644, BRACE3041059, BRACE3041162, BRACE3042046,
 25 BRACE3042432, BRACE3043597, BRACE3044172, BRACE3046152,
 BRACE3046466, BRACE3046609, BRACE3051621, BRACE3052321,
 BRALZ2010842, BRALZ2013621, BRAMY2041384, BRAMY3000692,
 BRAMY3004126, BRAMY3007078, BRAMY3009491, BRAMY3011501,
 BRAMY3011581, BRAMY3014027, BRAMY3015086, BRAMY3017920,
 30 BRAWH2002333, BRAWH2012866, BRAWH2014053,
 BRAWH3001638, BRAWH3001783, BRAWH3004335, BRAWH3010602,
 BRAWH3011577, BRAWH3011623, BRAWH3017180, BRAWH3017259,
 BRAWH3018548, BRAWH3019026, BRAWH3021580, BRAWH3023156,
 BRAWH3023172, BRAWH3023415, BRAWH3024186, BRAWH3029385,
 35 BRAWH3029538, BRAWH3031342, BRAWH3032298, BRAWH3032571,
 BRAWH3033513, BRAWH3034668, BRAWH3034775, BRAWH3034890,

BRAWH3036334, BRAWH3038324, BRAWH3038827, BRAWH3040900,
 BRAWH3041492, BRAWH3041556, BRAWH3042438, BRAWH3042447,
 BRAWH3042772, BRAWH3043295, BRAWH3043623, BRAWH3044151,
 BRAWH3046424, BRAWH3047565, BRAWH3047644, BRAWH3049544,
 5 BRCAN2003269, BRCAN2006051, BRCAN2010665, BRCAN2020331,
 BRCAN2021325, BRCOC2012386, BRHIP2008756, BRHIP2023735,
 BRHIP2029529, BRHIP3001076, BRHIP3001481, BRHIP3003984,
 BRHIP3004215, BRHIP3004725, BRHIP3005037, BRHIP3005307,
 BRHIP3005673, BRHIP3005801, BRHIP3006449, BRHIP3007609,
 10 BRHIP3010289, BRHIP3011567, BRHIP3017146, BRHIP3017855,
 BRHIP3021019, BRHIP3023922, BRHIP3025795, BRHIP3027191,
 BRHIP3027651, BRHIP3028742, BRHIP3029409, BRHIP3030230,
 BRHIP3032374, BRHIP3035006, BRHIP3036715, BRHIP3037543,
 BRHIP3039509, BRSSN2004710, BRSTN2006466, BRSTN2008475,
 15 BRSTN2011961, BRSTN2012069, BRSTN2016918, BRTHA2019726,
 BRTHA2020721, BRTHA2020910, BRTHA2024712, BRTHA2025869,
 BRTHA2026071, BRTHA2026290, BRTHA2031917, BRTHA2033155,
 BRTHA2033683, BRTHA3003736, BRTHA3010135, BRTHA3010212,
 BRTHA3011187, BRTHA3011998, BRTHA3012265, BRTHA3014547,
 20 BRTHA3021708, BRTHA3021971, BRTHA3023403, BRTHA3026916,
 BRTHA3027957, CHONS2001287, CHONS2002829, COLON2001829,
 COLON2004911, COLON2005735, CTONG2001932, CTONG2010330,
 CTONG2011801, CTONG2014206, D9OST2004417, FCBBF3020030,
 FCBBF3021191, FCBBF3024911, FCBBF5000384, FEBRA2013570,
 25 FEBRA2026582, FEBRA2028457, FEKID2002637, FELNG2000720,
 FELNG2001953, HCASM2008154, JCMLC1000159, JCMLC2000273,
 JCMLC2002095, KIDNE2015987, N1ESE2000698, NETRP2000961,
 NETRP2003448, NETRP2004017, NETRP2008582, NT2RI3008179,
 NT2RI3009480, NT2RI3009524, NT2RP8003787, NT2RP8008057,
 30 NTONG2003805, OCBBF2004478, OCBBF2007039, OCBBF2018618,
 OCBBF2024589, OCBBF2030927, OCBBF2036019, OCBBF3001202,
 OCBBF3004487, OCBBF3008392, OCBBF3020263, OCBBF3022166,
 OCBBF3025475, OCBBF3025503, OCBBF3025630, OCBBF3026979,
 PEBLM2005615, PLACE5000492, PLACE6001933, PLACE6016030,
 35 PLACE7000266, PLACE7001759, PLACE7002303, PLACE7003985,
 PLACE7004103, PLACE7006090, PLACE7006268, PLACE7006498,

PLACE7007379, PLACE7009563, PLACE7009757, PLACE7009936,
 PLACE7011559, PLACE7012111, PLACE7014247, PLACE7016526,
 PUAEN2000594, SKNSH2007306, SMINT2011406, SMINT2011509,
 SMINT2014721, SPLEN2007689, SPLEN2012571, SPLEN2025012,
 5 SPLEN2028417, SPLEN2033996, SYNOV2003326, SYNOV4009139,
 T1ESE2000609, TESTI2005112, TESTI2007490, TESTI2009739,
 TESTI2023903, TESTI2030901, TESTI2034913, TESTI2052670,
 TESTI4001517, TESTI4001679, TESTI4002868, TESTI4003796,
 TESTI4003944, TESTI4004653, TESTI4005322, TESTI4005653,
 10 TESTI4007965, TESTI4017382, TESTI4017647, TESTI4018436,
 TESTI4020596, TESTI4021197, TESTI4021569, TESTI4021713,
 TESTI4023096, TESTI4026080, TESTI4028182, TESTI4031173,
 TESTI4032128, TESTI4032834, TESTI4032913, TESTI4033177,
 TESTI4036048, TESTI4039575, TESTI4039904, TESTI4041984,
 15 TESTI4046073, TESTI4047119, TESTI4049786, TESTI4049899,
 TESTI4051015, TESTI4052775, THYMU3002825, THYMU3008105,
 THYMU3012402, THYMU3012983, THYMU3013785, THYMU3014173,
 THYMU3014372, THYMU3014620, THYMU3016518, THYMU3020221,
 THYMU3020869, THYMU3021586, THYMU3021755, THYMU3022434,
 20 THYMU3023400, THYMU3025118, THYMU3026306, THYMU3026532,
 THYMU3027671, THYMU3032032, THYMU3032798, THYMU3033649,
 THYMU3033759, THYMU3037052, THYMU3037772, THYMU3038158,
 THYMU3038375, THYMU3040172, THYMU3040746, THYMU3040816,
 THYMU3040829, THYMU3043200, THYMU3047115, THYMU3047760,
 25 TKIDN2011160, TLIVE2007736, TLUNG2000654, TLUNG2001445,
 TLUNG2001600, TRACH2024730, TRACH3004424, TRACH3005173,
 TRACH3005191, TRACH3005699, TRACH3006379, TRACH3006800,
 TRACH3008042, TRACH3009008, TRACH3009701, TRACH3010079,
 TRACH3010167, TRACH3010342, TRACH3011282, TRACH3011313,
 30 TRACH3011503, TRACH3012891, TRACH3015951, TRACH3016455,
 TRACH3016805, TRACH3018524, TRACH3018907, TRACH3019058,
 TRACH3019621, TRACH3020769, TRACH3020930, TRACH3021023,
 TRACH3021373, TRACH3021778, TRACH3021883, TRACH3023373,
 TRACH3023960, TRACH3024081, TRACH3024671, TRACH3025346,
 35 TRACH3026283, TRACH3026299, TRACH3028441, TRACH3028597,
 TRACH3028837, TRACH3029670, TRACH3030855, TRACH3031660,

TRACH3031678, TRACH3032570, TRACH3034680, TRACH3036750,
 TRACH3037505, TRACH3038399, TATER2001433, UTERU2024042,
 UTERU2037423, UTERU3001946, UTERU3004635, UTERU3011398,
 UTERU3012293, UTERU3012414, UTERU3012999, UTERU3015011,
 5 UTERU3015299, UTERU3016308, UTERU3017441, UTERU3017626,
 UTERU3019708, UTERU3021850, UTERU3022588

The following 23 clones are also predicted to belong to the category of disease-related protein.

ADRGL2011190, BRACE3002184, BRACE3026993, BRACE3046450,
 10 BRAWH3013197, BRAWH3046240, BRCAN2019772, BRHIP3030064,
 BRTHA3024233, CTONG2002832, CTONG2003764, PROST2010326,
 TBAES2004105, TESTI2046536, TESTI4005158, TESTI4005500,
 THYMU3024602, THYMU3046350, TRACH1000193, TRACH3019290,
 TRACH3021066, UTERU2017492, UTERU2036507

15 In particular, hit data of the following 390 clones for Swiss-Prot, or nr or RefSeq corresponded to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human gene and disease database (the OMIM Number is shown in the parenthesis after the Clone Name).

20 ADIPS2000069(146900), ASTRO2015162(606106), ASTRO2016114(603899),
 ASTRO3000154(601594), BLADE2000256(140750), BRACE1000475(600696),
 BRACE2012838(605032), BRACE2012947(140580), BRACE2013009(605888),
 BRACE2016896(601421), BRACE2017397(115437), BRACE2023744(600763),
 BRACE2027382(606019), BRACE3001403(126141), BRACE3001973(600976),
 25 BRACE3002756(603143), BRACE3004767(182790), BRACE3009392(600229),
 BRACE3013418(182900), BRACE3018083(605268),
 BRACE3019941(600595), BRACE3020669(603917), BRACE3025719(605493),
 BRACE3026345(147470), BRACE3026802(605784), BRACE3028998(603063),
 BRACE3036283(602052), BRACE3039378(604100), BRACE3040644(603159),
 30 BRACE3041059(603486), BRACE3041162(194556), BRACE3042046(311030),
 BRACE3042432(192321), BRACE3043597(603704), BRACE3044172(601231),
 BRACE3046152(604950), BRACE3046466(604210;600105),
 BRACE3046609(606457), BRACE3051621(601313;173900),
 BRACE3052321(603050),
 35 BRALZ2010842(212138), BRALZ2013621(600712), BRAMY2041384(114070),
 BRAMY3000692(603971), BRAMY3004126(603071), BRAMY3007078(602410),

BRAMY3009491(600286), BRAMY3011501(602869), BRAMY3011581(601243),
 BRAMY3014027(194542), BRAMY3015086(602879), BRAMY3017920(600365),
 BRAMY3018248(605464), BRAWH2002333(171891), BRAWH2012866(185605),
 BRAWH2014053(604581), BRAWH3001638(605003), BRAWH3001783(605514),
 5 BRAWH3004335(603244), BRAWH3010602(603216),
 BRAWH3011577(601139), BRAWH3011623(164020), BRAWH3017180(601441),
 BRAWH3017259(603143), BRAWH3018548(193065), BRAWH3019026(602033),
 BRAWH3021580(179838), BRAWH3023156(137190), BRAWH3023172(603755),
 BRAWH3023415(604346), BRAWH3024186(179590), BRAWH3029385(602378),
 10 BRAWH3029538(600948), BRAWH3031342(603971), BRAWH3032298(601995),
 BRAWH3032571(603277), BRAWH3033513(604054;261510),
 BRAWH3034668(603486), BRAWH3034775(605800), BRAWH3034890(606265),
 BRAWH3036334(603971), BRAWH3038324(604249), BRAWH3038827(600574),
 BRAWH3040900(604265), BRAWH3041492(130500), BRAWH3041556(172460),
 15 BRAWH3042438(125855), BRAWH3042447(606323), BRAWH3042772(602878),
 BRAWH3043295(179030), BRAWH3043623(600976), BRAWH3044151(605421),
 BRAWH3046424(300272), BRAWH3047565(606277), BRAWH3047644(605216),
 BRAWH3049544(602273), BRCAN2003269(171060;602347),
 BRCAN2006051(604581), BRCAN2010665(603583), BRCAN2020331(604851),
 20 BRCAN2021325(114855), BRCOC2012386(602277), BRHIP2008756(605819),
 BRHIP2023735(601670), BRHIP2029529(189972), BRHIP3001076(604673),
 BRHIP3001481(176889), BRHIP3003984(603722;223900),
 BRHIP3004215(603294), BRHIP3004725(602075), BRHIP3005037(603526),
 BRHIP3005307(603197), BRHIP3005673(138385), BRHIP3005801(605704),
 25 BRHIP3006449(604275), BRHIP3007609(426000), BRHIP3010289(603130),
 BRHIP3011567(114207), BRHIP3017146(602878), BRHIP3017855(606406),
 BRHIP3021019(176879), BRHIP3023922(156570;250940),
 BRHIP3025795(603877), BRHIP3027191(601746), BRHIP3027651(604589),
 BRHIP3028742(602076), BRHIP3029409(604156), BRHIP3030230(602367),
 30 BRHIP3032374(603197), BRHIP3035006(604402), BRHIP3036715(142800),
 BRHIP3037543(602052), BRHIP3039509(601328), BRSSN2004710(600127),
 BRSTN2006466(138275), BRSTN2008475(605178), BRSTN2011961(176790),
 BRSTN2012069(130590), BRSTN2016918(137780), BRTHA2019726(147100),
 BRTHA2020721(147100), BRTHA2020910(602661), BRTHA2024712(600747),
 35 BRTHA2025869(162280), BRTHA2026071(605297), BRTHA2026290(602306),
 BRTHA2031917(118946), BRTHA2033155(601873), BRTHA2033683(111000),

BRTHA3003736(133510;234050), BRTHA3010135(179590),
 BRTHA3010212(603971), BRTHA3011187(605837), BRTHA3011998(603264),
 BRTHA3012265(605646), BRTHA3014547(182900), BRTHA3021708(602654),
 BRTHA3021971(605609), BRTHA3023403(600597), BRTHA3026916(601619),
 5 BRTHA3027957(606078), CHONS2001287(146732), CHONS2002829(602981),
 COLON2001829(604399), COLON2004911(603937;180100),
 COLON2005735(111690;111700), CTONG2001932(605683),
 CTONG2010330(606088), CTONG2011801(603971), CTONG2014206(605609),
 D9OST2004417(113703), FCBBF3020030(603406), FCBBF3021191(605119),
 10 FCBBF5000384(601737), FEBRA2013570(248600), FEBRA2026582(300252),
 FEBRA2028457(164035), FEKID2002637(176875), FELNG2000720(601662),
 FELNG2001953(603597),
 HCASM2008154(133450), JCMLC1000159(107470;209950),
 JCMLC2000273(120980), JCMLC2002095(600738), KIDNE2015987(191845),
 15 N1ESE2000698(604734), NETRP2000961(600417), NETRP2003448(179551),
 NETRP2004017(605344), NETRP2008582(103195), NT2RI3008179(603808),
 NT2RI3009480(601804), NT2RI3009524(604210;600105),
 NT2RP8003787(605427), NT2RP8008057(603489), NTONG2003805(601781),
 OCBBF2004478(604265), OCBBF2007039(605009), OCBBF2018618(102775),
 20 OCBBF2024589(602462),
 OCBBF2030927(603897), OCBBF2036019(601825;256000),
 OCBBF3001202(140750), OCBBF3004487(142560), OCBBF3008392(605682),
 OCBBF3020263(604077), OCBBF3022166(600848), OCBBF3025475(604148),
 OCBBF3025503(601653;113650), OCBBF3025630(604141),
 25 OCBBF3026979(602319), PEBLM2005615(600242), PLACE5000492(602142),
 PLACE6001933(131550), PLACE6016030(605442), PLACE7000266(188840),
 PLACE7001759(600338), PLACE7002303(601542;180500;137600;604229),
 PLACE7003985(109684), PLACE7004103(142695),
 PLACE7006090(154360), PLACE7006268(603053), PLACE7006498(604394),
 30 PLACE7007379(603105), PLACE7009563(300344), PLACE7009757(601804),
 PLACE7009936(600365), PLACE7011559(600831), PLACE7012111(602714),
 PLACE7014247(601232), PLACE7016526(605490), PUAEN2000594(604679),
 SKNSH2007306(118990), SMINT2011406(147890), SMINT2011509(606343),
 SMINT2014721(606090), SPLEN2007689(233700), SPLEN2012571(603430),
 35 SPLEN2025012(146900), SPLEN2028417(142995),
 SPLEN2033996(603853), SYNOV2003326(602960), SYNOV4009139(603551),

T1ESE2000609(182465), TESTI2005112(603846), TESTI2007490(601291),
 TESTI2009739(160745), TESTI2023903(605046), TESTI2030901(600436),
 TESTI2034913(148060), TESTI2052670(142461), TESTI4001517(148070),
 TESTI4001679(602850), TESTI4002868(601863;209920),
 5 TESTI4003796(603132), TESTI4003944(603971), TESTI4004653(606106),
 TESTI4005322(603899), TESTI4005653(182465), TESTI4007965(603533),
 TESTI4017382(605689), TESTI4017647(603211), TESTI4018436(601754),
 TESTI4020596(602537), TESTI4021197(602189), TESTI4021569(605464),
 TESTI4021713(604105), TESTI4023096(604878), TESTI4026080(605575),
 10 TESTI4028182(603892), TESTI4031173(190197), TESTI4032128(104776),
 TESTI4032834(300188), TESTI4032913(106410), TESTI4033177(602038),
 TESTI4036048(601272), TESTI4039575(600951), TESTI4039904(603899),
 TESTI4041984(604710), TESTI4046073(300118;309801),
 TESTI4047119(606202), TESTI4049786(142600;235700),
 15 TESTI4049899(601969), TESTI4051015(602974), TESTI4052775(165250),
 THYMU3002825(604346), THYMU3008105(194548), THYMU3012402(600686),
 THYMU3012983(194556), THYMU3013785(604722), THYMU3014173(143010),
 THYMU3014372(116945), THYMU3014620(605657), THYMU3016518(147100),
 THYMU3020221(147100), THYMU3020869(602550), THYMU3021586(184756),
 20 THYMU3021755(605024), THYMU3022434(601408), THYMU3023400(605180),
 THYMU3025118(155735), THYMU3026306(604346),
 THYMU3026532(600065;116920), THYMU3027671(604143),
 THYMU3032032(604463), THYMU3032798(601212), THYMU3033649(186780),
 THYMU3033759(600495), THYMU3037052(300346), THYMU3037772(147100),
 25 THYMU3038158(603033;603034), THYMU3038375(181590),
 THYMU3040172(186720), THYMU3040746(147110), THYMU3040816(605704),
 THYMU3040829(602649), THYMU3043200(605596), THYMU3047115(108730),
 THYMU3047760(604783), TKIDN2011160(605011),
 TLIVE2007736(604990), TLUNG2000654(148059), TLUNG2001445(146900),
 30 TLUNG2001600(147130), TRACH2024730(605611), TRACH3004424(603971),
 TRACH3005173(151410), TRACH3005191(605333), TRACH3005699(606154),
 TRACH3006379(148059), TRACH3006800(606154), TRACH3008042(166945),
 TRACH3009008(601112), TRACH3009701(603330), TRACH3010079(604850),
 TRACH3010167(601804), TRACH3010342(602943), TRACH3011282(601833),
 35 TRACH3011313(113520), TRACH3011503(602862),
 TRACH3012891(602397), TRACH3015951(604084), TRACH3016455(605286),

TRACH3016805 (106410), TRACH3018524 (176882), TRACH3018907 (146900),
 TRACH3019058 (147170), TRACH3019621 (191350), TRACH3020769 (160776),
 TRACH3020930 (147100), TRACH3021023 (147170), TRACH3021373 (606030),
 TRACH3021778 (164035), TRACH3021883 (603347), TRACH3023373 (159350),
 5 TRACH3023960 (603337), TRACH3024081 (605867), TRACH3024671 (605942),
 TRACH3025346 (603377;212140), TRACH3026283 (601517),
 TRACH3026299 (147170), TRACH3028441 (147170), TRACH3028597 (604310),
 TRACH3028837 (602127), TRACH3029670 (147170), TRACH3030855 (173321),
 TRACH3031660 (176912), TRACH3031678 (600523), TRACH3032570 (602217),
 10 TRACH3034680 (147170), TRACH3036750 (604077), TRACH3037505 (147170),
 TRACH3038399 (604032;226980), TUTER2001433 (146900),
 UTERU2024042 (602214), UTERU2037423 (604077), UTERU3001946 (606154),
 UTERU3004635 (103390), UTERU3011398 (120240;158810;254090),
 UTERU3012293 (194556),
 15 UTERU3012414 (604394), UTERU3012999 (605567), UTERU3015011 (602505),
 UTERU3015299 (601825;256000), UTERU3016308 (602127),
 UTERU3017441 (604276), UTERU3017626 (603788), UTERU3019708 (601430),
 UTERU3021850 (605009), UTERU3022588 (123811)

Additionally, hit data of the following 23 clones for
 20 Swiss-Prot, nr or RefSeq corresponded to genes or proteins which
 had been deposited in the Online Mendelian Inheritance in Man
 (OMIM), which is the human gene and disease database (the OMIM
 Number is shown in the parenthesis after the Clone Name).

ADRGL2011190 (602658), BRACE3002184 (603899), BRACE3026993
 25 (601282), BRACE3046450 (603035), BRAWH3013197 (604100),
 BRAWH3046240 (602646), BRCAN2019772 (603849), BRHIP3030064
 (605762), BRTHA3024233 (603088), CTONG2002832 (604668),
 CTONG2003764 (176977), PROST2010326 (604110), TBAES2004105
 (605008), TESTI2046536 (182890; 182882), TESTI4005158 (601328),
 30 TESTI4005500 (602277), THYMU3024602 (600493), THYMU3046350
 (603080), TRACH1000193 (139139), TRACH3019290 (603975),
 TRACH3021066 (164870), UTERU2017492 (602917), UTERU2036507
 (605008)

The clones predicted to belong to the category of enzyme
 35 and/or metabolism-related protein are the following 164 clones.

ASTRO2008972, BRACE1000475, BRACE2013132, BRACE2016896,
BRACE2035120, BRACE3017253, BRACE3021805, BRACE3028998,
BRACE3031315, BRACE3036283, BRACE3041059, BRACE3042409,
BRACE3044172, BRACE3046609, BRAMY3009491, BRAMY3011581,
5 BRAWH2002333, BRAWH2014053, BRAWH3001638, BRAWH3004335,
BRAWH3011331, BRAWH3017180, BRAWH3020928, BRAWH3023415,
BRAWH3023421, BRAWH3024186, BRAWH3024506, BRAWH3029385,
BRAWH3029806, BRAWH3032571, BRAWH3033513, BRAWH3034668,
BRAWH3037428, BRAWH3037979, BRAWH3041556, BRAWH3042438,
10 BRAWH3043295, BRAWH3044151, BRAWH3046424, BRAWH3047692,
BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402,
BRCAN2021325, BRHIP3001481, BRHIP3003126, BRHIP3005307,
BRHIP3005673, BRHIP3007195, BRHIP3007223, BRHIP3011082,
BRHIP3011269, BRHIP3021019, BRHIP3023922, BRHIP3032374,
15 BRHIP3035006, BRHIP3037543, BRHIP3041587, BRSSN2004710,
BRSTN2006466, BRSTN2011961, BRTHA2005448, BRTHA2010672,
BRTHA2025869, BRTHA2026311, BRTHA2033155, BRTHA2035743,
BRTHA3003736, BRTHA3010135, BRTHA3010469, BRTHA3023403,
CHONS2002829, COLON2004351, CTONG2010330, CTONG2020582,
20 CTONG3001605, FCBBF3001018, FCBBF3021191, FCBBF5000384,
FEBRA2013570, FEBRA2026582, FEKID2002637, HSYRA2004550,
KIDNE2010049, NETRP2000961, NT2RI2004818, NT2RP7016508,
OCBBF2007039, OCBBF2024589, OCBBF2036019, OCBBF3004487,
OCBBF3005330, OCBBF3009244, PLACE5000492, PLACE6001933,
25 PLACE7001759, PLACE7003985, PLACE7004103, PLACE7004961,
PLACE7006090, PLACE7006268, PLACE7007379, PLACE7011559,
PLACE7012111, PLACE7014247, PLACE7016526, SKMUS2008585,
SMINT2011509, SMINT2012179, SMINT2014721, SPLEN2007689,
SYNOV4009139, TBAES2007428, TESTI2005112, TESTI2007490,
30 TESTI2021654, TESTI2040377, TESTI2049062, TESTI4000621,
TESTI4002799, TESTI4007671, TESTI4020596, TESTI4033177,
TESTI4049786, TESTI4052219, THYMU3002825, THYMU3026306,
THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428,
THYMU3047115, THYMU3047891, TKIDN2011160, TRACH3005173,
35 TRACH3005274, TRACH3009008, TRACH3011313, TRACH3011503,
TRACH3012891, TRACH3015136, TRACH3016455, TRACH3018108,

TRACH3018261, TRACH3018524, TRACH3019621, TRACH3021544,
 TRACH3022758, TRACH3023516, TRACH3024020, TRACH3024081,
 TRACH3027229, TRACH3027701, TRACH3032150, TRACH3038399,
 TSTOM2001571, TSTOM2002611, UTERU2024042, UTERU3010604,
 5 UTERU3010919, UTERU3015299, UTERU3019708, UTERU3021850

The following eight clones are also predicted to belong to the category of enzyme and/or metabolism-related protein.

ADRGL2011190, BRHIP3030064, CTONG2003764, PLACE7013963,
 TBAES2004105, THYMU3044175, TRACH3021066, UTERU2036507

10 The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 27 clones.

BLADE2000256, BRACE2002392, BRACE3030538, BRACE3036283,
 BRACE3044495, BRAMY3002886, BRAMY3009556, BRAWH2016209,
 15 BRAWH3004350, BRAWH3027574, BRCAN2019907, BRHIP3001076,
 BRHIP3029409, BRSTN2008475, BRTHA3011265, FEKID2002637,
 NT2RP8005546, OCBBF3001202, PLACE7011559, SPLEN2033996,
 TESTI2023903, TESTI4020819, TESTI4049899, THYMU3014372,
 THYMU3021586, UTERU3010919, UTERU3012999

20 The following two clones are also predicted to belong to the category of cell division and/or cell proliferation-related protein.

TBAES2007481, TESTI2046536

25 The clones predicted to belong to the category of cytoskeleton-related protein are the following 60 clones.

BRACE3004767, BRACE3013418, BRACE3051819, BRAMY3005184,
 BRAMY3015086, BRAMY4000915, BRAMY4001652, BRAWH3001783,
 BRAWH3015175, BRAWH3018548, BRAWH3019026, BRAWH3021580,
 BRAWH3021724, BRAWH3027440, BRAWH3027806, BRAWH3029385,
 30 BRAWH3040900, BRAWH3041492, BRCAN2020467, BRHIP3003063,
 BRHIP3003340, BRSTN2016918, BRTHA2020910, BRTHA2025869,
 BRTHA3014547, BRTHA3025073, CERVX2000968, JCMLC2000273,
 N1ESE2000698, NT2RI3005923, OCBBF2003518, OCBBF2004478,
 OCBBF3027969, PLACE7000266, PLACE7004961, SMINT2010753,
 35 SPLEN2034934, SYNOV4003174, TESTI2001915, TESTI2009739,
 TESTI2034913, TESTI4001517, TESTI4004917, TESTI4010902,

TESTI4032913, TESTI4051424, THYMU3026532, TLUNG2000654,
 TRACH3006379, TRACH3016805, TRACH3020769, TRACH3022960,
 TRACH3026650, TRACH3028837, TRACH3029462, TRACH3032570,
 UTERU3000670, UTERU3001029, UTERU3015011, UTERU3016308

5 The following one clone is also predicted to belong to the
 category of cytoskeleton-related protein.

BRACE3026993

10 The clones predicted to belong to the category of nuclear
 protein and/or RNA synthesis-related protein are the following
 40 clones.

ASTRO3000154, BRACE3014714, BRACE3036283, BRALZ2013621,
 BRAMY3009556, BRAMY3011501, BRAWH3011623, BRAWH3017180,
 BRAWH3022651, BRAWH3038252, BRAWH3040695, BRAWH3046424,
 BRHIP3004215, BRHIP3007223, BRHIP3020046, BRTHA3010530,
 15 CTONG2006235, FEBRA2028457, NT2RP7016508, OCBBF3001333,
 OCBBF3004487, PLACE7004103, PLACE7006268, TESTI2036285,
 TESTI2037657, TESTI4014932, TESTI4028182, TESTI4032128,
 TESTI4033177, TESTI4039575, THYMU3012402, THYMU3040829,
 THYMU3041428, TRACH3002752, TRACH3018108, TRACH3021778,
 20 UTERU3004635, UTERU3010409, UTERU3010919, UTERU3013302

The following one clone is also predicted to belong to the
 category of nuclear protein and/or RNA synthesis-related protein.
 TESTI2046536

25 The clones predicted to belong to the category of protein
 synthesis and/or transport-related protein are the following 50
 clones.

BRACE2016896, BRACE2023744, BRACE3020669, BRACE3030538,
 BRACE3041059, BRACE3043597, BRAWH2014053, BRAWH3001638,
 BRAWH3010602, BRAWH3024506, BRAWH3026349, BRAWH3034668,
 30 BRAWH3037979, BRAWH3041556, BRAWH3044151, BRAWH3047692,
 BRCAN2000923, BRCAN2002892, BRCAN2006051, BRCAN2021325,
 BRHIP3007223, BRSTN2012069, BRTHA2005448, BRTHA2010672,
 CHONS2002829, CTONG3001605, D9OST2004417, OCBBF2000831,
 OCBBF2007039, PLACE6019600, PLACE7007379, PLACE7012111,
 35 PLACE7016526, TESTI4018436, TESTI4020596, TESTI4032128,
 TESTI4036048, THYMU3012402, THYMU3033759, THYMU3036953,

THYMU3046360, TKIDN2011160, TRACH3016455, TRACH3018519,
 TRACH3021544, TRACH3025316, TRACH3030855, TRACH3038399,
 UTERU3014647, UTERU3021850

The following two clones are also predicted to belong to
 5 the category of protein synthesis and/or transport-related
 protein.

TBAES2004105, UTERU2036507

The clones predicted to belong to the category of cellular
 defense-related protein are the following five clones.

10 BRACE2012947, BRHIP2029529, BRTHA3003736, THYMU3015571,
 TRACH3022296

The clones predicted to belong to the category of
 development and/or differentiation-related protein are the
 following 16 clones.

15 ASTRO3000154, BRACE3034964, BRAWH3004350, BRAWH3029538,
 BRAWH3038252, BRHIP3007424, BRTHA2024712, BRTHA3011265,
 FEKID2002493, NT2RP8003490, NT2RP8006452, OCBBF3025503,
 PLACE7002303, TESTI2026024, TRACH3028180, UTERU3016070

The following one clone is also predicted to belong to the
 20 category of development and/or differentiation-related protein.
 BRCAN2019772

The clones predicted to belong to the category of DNA-
 binding and/or RNA-binding protein are the following 119 clones.

ASTRO2016114, BEAST2000981, BRACE2012947, BRACE2019348,
 25 BRACE3020669, BRACE3025719, BRACE3026844, BRACE3031743,
 BRACE3034183, BRACE3041162, BRACE3046152, BRALZ2013621,
 BRAMY2040915, BRAMY2046537, BRAMY3000692, BRAMY3007078,
 BRAMY3011501, BRAMY3011581, BRAMY3014027, BRAMY3018754,
 BRAMY4000962, BRAWH3000446, BRAWH3011577, BRAWH3011623,
 30 BRAWH3013009, BRAWH3013264, BRAWH3017477, BRAWH3028796,
 BRAWH3031342, BRAWH3032571, BRAWH3034775, BRAWH3035936,
 BRAWH3036247, BRAWH3036334, BRAWH3038827, BRCAN2020331,
 BRCOC2012386, BRHIP2027077, BRHIP3004725, BRHIP3028246,
 BRSSN2015497, BRTHA2024712, BRTHA3000456, BRTHA3003736,
 35 BRTHA3010212, BRTHA3014000, BRTHA3028339, CHONS2000797,
 CHONS2002829, CTONG2001932, CTONG2011801, D9OST2003106,

FCBBF3020030, FCBBF5000384, FEBRA2028457, HCASM2008154,
 NETRP2004017, NT2RI3008179, NT2RI3009480, NT2RP7016508,
 NT2RP8003490, NTONG2003805, NTONG2008483, OCBBF2016928,
 OCBBF3004487, OCBBF3008392, OCBBF3020263, OCBBF3021361,
 5 OCBBF3022166, PLACE7002303, PLACE7004103, PLACE7005169,
 PLACE7009757, PROST2002078, PUAEN2000594, SMINT2011509,
 SPLEN2012571, SPLEN2028417, T1ESE2000609, T1ESE2000904,
 TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322,
 TESTI4005470, TESTI4005653, TESTI4032128, TESTI4039575,
 10 TESTI4039904, TESTI4052775, THYMU3008105, THYMU3012983,
 THYMU3014372, THYMU3020869, THYMU3021586, THYMU3026000,
 THYMU3030072, THYMU3033759, THYMU3037052, THYMU3040829,
 TLIVE2001616, TRACH3003458, TRACH3004424, TRACH3005191,
 TRACH3008508, TRACH3010079, TRACH3010167, TRACH3010342,
 15 TRACH3015951, TRACH3021778, TRACH3021883, TRACH3022109,
 TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293,
 UTERU3013302, UTERU3016070, UTERU3022588

The following eight clones are also predicted to belong to the category of DNA-binding and/or RNA-binding protein.

20 BRACE3002184, BRCAN2019772, CTONG2002832, TESTI2046536,
 TESTI4002988, TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 68 clones.

BRACE2013009, BRACE2016896, BRACE3002344, BRACE3014714,
 25 BRACE3017253, BRACE3036283, BRACE3051819, BRAMY3011501,
 BRAMY3018248, BRAWH2014053, BRAWH3015175, BRAWH3024506,
 BRAWH3029385, BRAWH3032571, BRAWH3037428, BRAWH3041556,
 BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2003269,
 BRCAN2006051, BRHIP3007195, BRHIP3027191, BRHIP3041587,
 30 BRSTN2012069, BRTHA2020910, BRTHA3003736, HSYRA2004550,
 KIDNE2010049, NETRP2003448, NT2RP7016508, OCBBF2003518,
 OCBBF3004487, PLACE6001933, PLACE6019600, PLACE7004961,
 PLACE7006498, PLACE7011559, PLACE7016526, PUAEN2006639,
 SMINT2011406, TESTI2009739, TESTI2040377, TESTI4004917,
 35 TESTI4013474, TESTI4021569, TESTI4028182, TESTI4049786,
 TESTI4052219, THYMU3014372, THYMU3032798, THYMU3041428,

THYMU3047115, TRACH3005191, TRACH3009061, TRACH3009701,
 TRACH3012891, TRACH3019370, TRACH3020769, TRACH3022960,
 TRACH3023960, TRACH3024081, TRACH3038399, TSTOM2001571,
 UTERU2024042, UTERU3010919, UTERU3012414, UTERU3019708

- 5 The following two clones are also predicted to belong to
 the category of ATP binding and/or GTP-binding protein.

CTONG2003764, TRACH3021066

- 10 The 104 clones shown below are clones which were
 unassignable to any of the above-mentioned categories, but have
 been predicted to have some function based on homology search
 using their full-length nucleotide sequences. Clone Name and
 Definition in the result of homology search, demarcated by a
 double slash mark (//), are shown below.

- BLADE2002310//SH3-domain binding protein 1 [Homo sapiens]
 15 BLADE2007799//Hepatocellular carcinoma-associated antigen 66.
 BRACE2017359//Mus musculus suppressor of Ty 6 homolog (S.
 cerevisiae) (Supt6h)
 BRACE2017872//nuclear receptor-binding SET-domain protein 1 [Mus
 musculus]
 20 BRACE3009416//testis specific ankyrin-like protein 1 [Homo
 sapiens]
 BRACE3016020//SBBI31 protein [Homo sapiens]
 BRACE3019570//SNAP-25-interacting protein [Rattus norvegicus]
 BRACE3022303//Pax transcription activation domain interacting
 25 protein [Mus musculus]
 BRACE3022340//SNAP-25-interacting protein [Rattus norvegicus]
 BRACE3026290//Homo sapiens lethal giant larvae homolog 2 [Homo
 sapiens]
 BRACE3032631//F-box protein FBX13 [Mus musculus].
 30 BRACE3040239//Deltex3 [Mus musculus]
 BRACE3047482//tripartite motif-containing 9 [Homo sapiens]
 BRACE3049714//NYD-TSPG protein [Homo sapiens]
 BRACE3052410//IDN3 protein [Homo sapiens]
 BRACE3052595//Nim2 [Rattus norvegicus]
 35 BRALZ2014054//cenexin 2 [Rattus norvegicus].
 BRAMY3007471//gene trap locus F3b; transcript expressed during

hematopoiesis 2 [Mus musculus]
 BRAMY3010321//MRIP-1 protein [Homo sapiens]
 BRAMY3014613//SH3-domain binding protein 1 [Homo sapiens]
 BRAMY4001863//Mus musculus enabled homolog (Drosophila) (Enah),
 5 mRNA
 BRAWH2011796//S-100 protein, alpha chain.
 BRAWH3008167//CUB and Sushi multiple domains 1 [Homo sapiens]
 BRAWH3009961//Nim2 [Rattus norvegicus]
 BRAWH3010726//phosphatidylinositol transfer protein, membrane-
 10 associated; Drosophila retinal degeneration B [Homo sapiens]
 BRAWH3015017//axonemal dynein light chain p33.
 BRAWH3024231//Tetratricopeptide repeat protein 4.
 BRAWH3026938//semaF cytoplasmic domain associated protein 3;
 semaphorin cytoplasmic domain-associated protein 3A [Mus
 15 musculus]
 BRAWH3027533//rap2 interacting protein x [Homo sapiens].
 BRAWH3030910//Sec23-interacting protein p125 [Homo sapiens]
 BRAWH3031710//serologically defined colon cancer antigen 33
 [Homo sapiens]
 20 BRAWH3033293//synaptopodin [Homo sapiens]
 BRAWH3042568//ventral anterior homeobox containing gene 1 [Mus
 musculus]
 BRAWH3043034//Mus musculus neuregulin 1 (Nrg1)
 BRAWH3044122//Munc13-1 [Rattus norvegicus]
 25 BRHIP2026346//lymphocyte specific formin related protein;
 formin-related gene in leukocytes [Mus musculus]
 BRHIP2027563//host cell factor homolog [Homo sapiens]
 BRHIP3002114//rTS beta protein [Homo sapiens]
 BRHIP3003795//cytochrome P450 retinoid metabolizing protein
 30 [Homo sapiens]
 BRHIP3006786//peptidylprolyl isomerase (cyclophilin)-like 2;
 cyclophilin-like protein CyP-60 [Homo sapiens]
 BRHIP3017109//Socs-5 [Mus musculus]
 BRHIP3019643//Homo sapiens gamma tubulin ring complex protein
 35 (76p gene) (76P), mRNA
 BRHIP3032148//brain-enriched guanylate kinase-associated [Rattus

norvegicus]
 BRSTN2006638//synaptotagmin interacting protein 1 [Rattus
 norvegicus]
 BRSTN2016892//BUP protein [Homo sapiens]
 5 BRSTN2016992//DRR1 protein (TU3A protein).
 BRSTN2017151//COP9 (constitutive photomorphogenic), subunit 7a
 (Arabidopsis); COP9 complex S7a [Mus musculus]
 BRTHA2020642//DRR1 protein (TU3A protein).
 BRTHA3018409//synaptotagmin-like 4; granuphilin-a; granuphilin-
 10 b; granuphilin
 BRTHA3019183//<Ca2+>dependent activator protein for secretion;
 Ca2+-dependent activator protein for secretion [Mus musculus]
 CHONS2001834//tumor endothelial marker 7 precursor [Homo
 sapiens]
 15 CTONG2009570//rab11 binding protein [Bos taurus].
 CTONG2012123//Mus musculus enabled homolog (Drosophila) (Enah),
 mRNA
 CTONG2027591//Mus musculus pecanex homolog (Drosophila) (Pcnx),
 mRNA.
 20 CTONG3003669//high-glucose-regulated protein 8 [Homo sapiens]
 ERLTF2002178//Kelch-like protein X.
 HHDPC2008185//jerky [Mus musculus]
 NT2RI3001573//F-box protein FBL10 [Mus musculus].
 NT2RI3007095//Mus musculus neuregulin 1 (Nrg1), mRNA.
 25 NT2RP8001363//signal peptide, CUB domain, EGF-like 1 [Mus
 musculus]
 NT2RP8001584//alpha integrin binding protein 63 [Homo sapiens]
 NT2RP8001604//CUB and Sushi multiple domains 1 [Homo sapiens]
 OCBBF3019269//Homo sapiens Dvl-binding protein IDAX (inhibition
 30 of the Dvl and Axin complex) (IDAX)
 OCBBF3022827//putative Rab5 GDP/GTP exchange factor homologue
 [Homo sapiens]
 OCBBF3023913//Mus musculus protein phosphatase 1, regulatory
 (inhibitor) subunit 1C (Ppp1r1c)
 35 PLACE6003004//rTS beta protein [Homo sapiens]
 PLACE6008315//similar to ALPHA-ACTININ, SARCOMERIC (F-ACTIN

CROSS LINKING PROTEIN) (D. melanogaster) [Homo sapiens].
 PLACE6010925//NY-REN-50 antigen [Homo sapiens]
 PLACE7012127//AAA-ATPase TOB3 [Homo sapiens]
 PROST2016566//erythroblast macrophage protein [Mus musculus]
 5 SYNOV2017179//EBP50-PDZ interactor of 64 kD [Homo sapiens]
 SYNOV3000345//upregulated by 1,25-dihydroxyvitamin D-3 [Homo sapiens]
 TBAES2003917//NG28 protein [Mus musculus]
 TESTI2001364//lactate dehydrogenase A -like [Homo sapiens]
 10 TESTI2004601//NYD-TSPG protein [Homo sapiens]
 TESTI2009497//GPI-anchored protein p137 (p137GPI).
 TESTI4002774//oxysterol binding protein 2 [Mus musculus]
 TESTI4003579//FH1/FH2 domains-containing protein (Formin homolog overexpressed in spleen) (FHOS).
 15 TESTI4003703//retinoblastoma-associated protein RAP140 [Homo sapiens]
 TESTI4013742//antigen identified by monoclonal antibody 2A8 [Mus musculus]
 TESTI4014908//dedicator of cyto-kinesis 2 [Mus musculus]
 20 TESTI4018506//tomosyn [Rattus norvegicus]
 TESTI4020342//H326 [Homo sapiens]
 TESTI4024294//WW domain binding protein 2 [Mus musculus]
 TESTI4039451//B29 protein [Homo sapiens]
 TESTI4041482//Rattus norvegicus SEC15 homolog (S. cerevisiae)
 25 (Sec15), mRNA
 TESTI4043166//lymphocyte specific formin related protein; formin-related gene in leukocytes [Mus musculus]
 TESTI4047328//otogelin [Mus musculus]
 THYMU3011717//exocyst component protein 70 kDa homolog (S. cerevisiae)
 30
 THYMU3016822//erythroblast macrophage protein [Mus musculus]
 THYMU3026479//secretory pathway component Sec31B-1 [Homo sapiens]
 THYMU3028702//chromosome condensation-related SMC-associated
 35 protein 1; chromosome condensation-related SMC-associated protein 1; KIAA0159 gene product [Homo sapiens]

THYMU3029719//AAA-ATPase TOB3 [Homo sapiens]
 THYMU3038347//tumor stroma and activated macrophage protein DLM-
 1 [Homo sapiens]
 THYMU3038603//WW domain binding protein 2 [Mus musculus]
 5 THYMU3040830//AD-012 protein [Homo sapiens]
 THYMU3041603//gamma-tubulin complex protein 2 [Homo sapiens]
 TKIDN2003396//Homo sapiens paternally expressed 10 (PEG10), mRNA
 TRACH2011057//D-type cyclin-interacting protein 1; MAID protein
 [Homo sapiens]
 10 TRACH3004412//clusterin-like 1 (retinal); unknown prepropeptide
 specific to rod photoreceptor [Homo sapiens]
 TRACH3012106//erythrocyte protein band 4.1-like 3 [Mus musculus]
 UTERU3009775//PAPIN [Rattus norvegicus]
 UTERU3010892//adaptor-related protein complex 3, delta 1
 15 subunit; adaptin, delta [Homo sapiens]
 UTERU3017995//p47 [Homo sapiens]

So far no information suggesting the function of the
 following six clones has been provided by the homology search.
 The functions of these clones may be clarified when an updated
 20 database becomes available in future. Clone names are shown
 below.

BRAMY3008096, BRAMY3016953, BRHIP3038037, BRTHA3004432,
 TESTI4052089, UTERU3020583

25 Further, a polypeptide will not always belong solely to a
 single category of the above-described functional categories,
 and therefore, a polypeptide may belong to any of the predicted
 functional categories. Further analyses may yield additional
 functions for clones classified into these functional categories.

30 Detailed descriptions concerning each domain or motif can
 be found in websites linked from the websites of Pfam, InterPro
 (<http://www.ebi.ac.uk/interpro/>), PROSITE
 (<http://www.expasy.ch/cgi-bin/prosite-list.pl>), or such. This
 information can be found based on domain/motif names, and
 35 accession numbers of hit data obtained through domain searches
 of Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) (see

Example 5) for amino acid sequences deduced from the 2,495 full-length clones of the present invention whose full-length nucleotide sequences have been determined. PROSITE in particular enables comparison of unique functional categories.

5 The functions of polypeptides encoded by the 825 clones with hit data in Pfam were predicted and classified into the 14 functional categories described below. As a result, 646 clones were estimated to encode proteins belonging to these categories.

Secretory and/or membrane protein (102 clones)

10 Glycoprotein-related protein (83 clones)

Signal transduction-related protein (128 clones)

Transcription-related protein (149 clones)

Disease-related protein (four clones)

Enzyme and/or metabolism-related protein (271 clones)

15 Cell division- and/or cell proliferation-related protein (14 clones)

Cytoskeleton-related protein (51 clones)

Nuclear protein and/or RNA synthesis-related protein (29 clones)

20 Protein synthesis- and/or transport-related protein (51 clones)

Cellular defense-related protein (four clones)

Development and/or differentiation-related protein (one clone)

25 DNA- and/or RNA-binding protein (192 clones)

ATP- and/or GTP-binding protein (42 clones)

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 92 clones.

3NB692004045, BRACE3002264, BRACE3009392, BRACE3013418,
30 BRACE3024879, BRACE3032385, BRACE3039378, BRACE3042432,
BRACE3050504, BRACE3051621, BRAMY2046537, BRAMY3004126,
BRAWH2000256, BRAWH2011812, BRAWH3023156, BRAWH3025157,
BRAWH3027880, BRAWH3036270, BRAWH3037265, BRAWH3042772,
BRCAN2003269, BRCAN2022126, BRCOC2006164, BRHIP3002000,
35 BRHIP3005944, BRHIP3008320, BRHIP3011567, BRHIP3014675,
BRHIP3016032, BRHIP3017558, BRHIP3025795, BRHIP3033557,

BRHIP3039509, BRSTN2010089, BRTHA2031917, BRTHA3011194,
 BRTHA3012265, BRTHA3014547, COLON2005735, JCMLC2000273,
 KIDNE2004531, LYMPB2002236, NT2RP7019682, NT2RP8001363,
 NT2RP8003787, OCBBF2003518, OCBBF2004478, OCBBF2009536,
 5 OCBBF2018618, OCBBF3004487, OCBBF3025475, OCBBF3028001,
 PEBLM2005615, PLACE6010936, PLACE7004103, PLACE7011559,
 PLACE7018304, TESTI2018335, TESTI2022323, TESTI2024267,
 TESTI2036822, TESTI4003602, TESTI4004539, TESTI4005399,
 TESTI4008305, TESTI4010544, TESTI4014415, TESTI4021569,
 10 TESTI4023096, TESTI4026080, TESTI4040559, TESTI4049899,
 THYMU3015647, THYMU3021404, THYMU3023400, THYMU3026532,
 THYMU3030752, THYMU3040172, THYMU3044075, TRACH3003357,
 TRACH3004113, TRACH3004747, TRACH3005699, TRACH3006800,
 TRACH3009061, TRACH3019370, TRACH3023373, TRACH3031678,
 15 TRACH3032150, UTERU3001946, UTERU3016273, UTERU3017626

The following ten clones are also predicted to belong to the category of secretory protein and/or membrane protein.

BRAWH3013197, BRAWH3028645, BRAWH3046240, BRCAN2019772,
 PROST2010326, TESTI2043585, TESTI4005158, THYMU3024602,
 20 THYMU3046350, TRACH1000193

The clones predicted to belong to the category of glycoprotein-related protein are the following 81 clones.

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3013874,
 BRACE3017253, BRACE3039358, BRAMY2040915, BRAMY3015549,
 25 BRAWH3009961, BRAWH3023415, BRAWH3049544, BRHIP3017558,
 BRHIP3025795, BRHIP3036371, BRHIP3036715, BRHIP3038735,
 BRTHA2019726, BRTHA2020400, BRTHA2020721, BRTHA3017791,
 CERVX2000968, FELNG2000720, JCMLC2000273, KIDNE2004531,
 NT2RP8008057, OCBBF2000831, OCBBF2004478, OCBBF2030927,
 30 PEBLM2005615, PLACE7006090, SPLEN2025012, STOMA2004663,
 TESTI2021654, TESTI2052670, TESTI4008305, TESTI4022158,
 TESTI4031173, TESTI4032128, TESTI4037949, TESTI4051424,
 THYMU3002825, THYMU3014173, THYMU3016518, THYMU3020221,
 THYMU3025118, THYMU3026306, THYMU3026532, THYMU3037772,
 35 THYMU3040746, TLUNG2001445, TLUNG2001600, TRACH3003357,
 TRACH3004113, TRACH3004412, TRACH3005274, TRACH3005699,

TRACH3006800, TRACH3011082, TRACH3011184, TRACH3012659,
 TRACH3015354, TRACH3018261, TRACH3018907, TRACH3019058,
 TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023,
 TRACH3024512, TRACH3026299, TRACH3028441, TRACH3029670,
 5 TRACH3031316, TRACH3034680, TRACH3036103, TRACH3037505,
 TUTER2001433, UTERU3001946, UTERU3010409, UTERU3011398,
 UTERU3015647

The following two clones are also predicted to belong to the category of glycoprotein-related protein.

10 BRAWH3028645, TESTI4005158

The clones predicted to belong to the category of signal transduction-related protein are the following 125 clones.

BLADE2002310, BLADE2008809, BRACE2047975, BRACE3002344,
 BRACE3003866, BRACE3004767, BRACE3013418, BRACE3015898,
 15 BRACE3017253, BRACE3042046, BRACE3044172, BRACE3045424,
 BRACE3046491, BRACE3051621, BRACE3052321, BRACE3052595,
 BRAMY3005184, BRAMY3009491, BRAMY3010321, BRAMY3014613,
 BRAMY3015547, BRAMY3017920, BRAWH2012866, BRAWH3009961,
 BRAWH3017180, BRAWH3018063, BRAWH3019026, BRAWH3022431,
 20 BRAWH3024186, BRAWH3026349, BRAWH3027574, BRAWH3027806,
 BRAWH3029385, BRAWH3031342, BRAWH3032340, BRAWH3035914,
 BRAWH3037428, BRAWH3044122, BRAWH3047692, BRCAN2000923,
 BRCAN2002892, BRCOC2001355, BRHIP3003306, BRHIP3006294,
 BRHIP3006786, BRHIP3011460, BRHIP3017109, BRHIP3021019,
 25 BRHIP3028570, BRHIP3037543, BRHIP3041587, BRTHA2026290,
 BRTHA2027250, BRTHA3014547, BRTHA3020771, BRTHA3021708,
 BRTHA3023403, BRTHA3026916, CTONG2009570, ERLTF2002369,
 FEKID2001001, FEKID2002637, FELNG2001953, KIDNE2010049,
 LYMPB2002344, N1ESE2000698, NETRP2003448, NT2RI2004818,
 30 NTONG2008483, OCBBF3006986, OCBBF3021086, OCBBF3021502,
 OCBBF3023175, PLACE5000492, PLACE6000055, PLACE6019600,
 PLACE7009936, PLACE7014247, PLACE7016526, PUAEN2006639,
 SKMUS2008585, SKMUS2009557, SMINT2017964, SPLEN2007689,
 SYNOV2017179, SYNOV4009575, TESTI4002774, TESTI4004695,
 35 TESTI4010902, TESTI4012960, TESTI4013474, TESTI4020342,
 TESTI4020596, TESTI4021197, TESTI4022158, TESTI4028042,

TESTI4029731, TESTI4033177, TESTI4036048, TESTI4046073,
 TESTI4047808, TESTI4049786, TESTI4051865, THYMU3013785,
 THYMU3025683, THYMU3032798, TRACH2024730, TRACH3003037,
 TRACH3003357, TRACH3005173, TRACH3011538, TRACH3018519,
 5 TRACH3020605, TRACH3024020, TRACH3030176, TRACH3031660,
 TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042,
 UTERU3001029, UTERU3006720, UTERU3010919, UTERU3021231,
 UTERU3022168

The following three clones are also predicted to belong to
 10 the category of signal transduction-related protein.
 BRAMY3008096, TESTI4052089, TRACH3021066

The clones predicted to belong to the category of
 transcription-related protein are the following 141 clones.
 ASTRO2016114, BEAST2000981, BRACE2019348, BRACE3025719,
 15 BRACE3026844, BRACE3026947, BRACE3029021, BRACE3034183,
 BRACE3040239, BRACE3041162, BRACE3047482, BRAMY2041347,
 BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027,
 BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209,
 BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3013009,
 20 BRAWH3013264, BRAWH3015175, BRAWH3015610, BRAWH3017477,
 BRAWH3021580, BRAWH3022651, BRAWH3027533, BRAWH3027880,
 BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3032571,
 BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3042787,
 BRAWH3044122, BRAWH3046424, BRCAN2021452, BRCOC2012386,
 25 BRHIP2027077, BRHIP2029663, BRHIP3005037, BRHIP3007609,
 BRHIP3017256, BRHIP3019824, BRHIP3027651, BRHIP3028246,
 BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA3000456,
 BRTHA3003225, BRTHA3010212, BRTHA3014000, BRTHA3028339,
 CHONS2000797, CTONG2006235, CTONG2011801, FCBBF3020030,
 30 FEBRA2002260, HCASM2008154, KIDNE2018268, NETRP2003103,
 NETRP2004017, NT2RI3009480, NTONG2003805, NTONG2008483,
 OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3008392,
 OCBBF3019269, OCBBF3020263, OCBBF3022827, OCBBF3025503,
 OCBBF3026361, PLACE7005169, PLACE7007973, PLACE7009757,
 35 PLACE7018512, SMINT2014721, SPLEN2012571, SPLEN2036608,
 TIESE2000904, TESTI2036822, TESTI2040377, TESTI4000370,

TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796,
 TESTI4003944, TESTI4005322, TESTI4005470, TESTI4024494,
 TESTI4028182, TESTI4032913, TESTI4039904, TESTI4051054,
 TESTI4052775, THYMU2008207, THYMU2038199, THYMU3008105,
 5 THYMU3012983, THYMU3014372, THYMU3021586, THYMU3022434,
 THYMU3026000, THYMU3030072, THYMU3034671, THYMU3037617,
 THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616,
 TLUNG2000654, TRACH3002752, TRACH3003037, TRACH3003458,
 TRACH3004113, TRACH3004412, TRACH3004424, TRACH3005274,
 10 TRACH3010079, TRACH3010167, TRACH3015951, TRACH3022109,
 TRACH3026303, TRACH3028180, TRACH3036750, UTERU2037423,
 UTERU3012293, UTERU3015011, UTERU3016070, UTERU3018172,
 UTERU3022588

The following eight clones are also predicted to belong to
 15 the category of transcription-related protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI2046536,
 TESTI4002988, TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of disease-
 related protein are the following four clones.

20 BRAWH3041928, BRHIP3000859, BRTHA3018409, THYMU3025642

The clones predicted to belong to the category of enzyme
 and/or metabolism-related protein are the following 264 clones.

BRACE1000475, BRACE2003628, BRACE2012528, BRACE2013132,
 BRACE2016896, BRACE2035120, BRACE2042541, BRACE2047975,
 25 BRACE3002344, BRACE3009392, BRACE3013418, BRACE3015898,
 BRACE3017253, BRACE3019941, BRACE3024444, BRACE3031315,
 BRACE3031372, BRACE3032537, BRACE3033525, BRACE3034183,
 BRACE3034964, BRACE3039288, BRACE3039454, BRACE3041059,
 BRACE3042409, BRACE3044172, BRACE3046491, BRACE3049714,
 30 BRACE3050270, BRACE3051819, BRACE3052410, BRACE3052595,
 BRAMY3007078, BRAMY3009491, BRAMY3011581, BRAMY3014613,
 BRAMY4000915, BRAWH2000256, BRAWH2002333, BRAWH2012866,
 BRAWH2014053, BRAWH2016785, BRAWH3009961, BRAWH3010657,
 BRAWH3013264, BRAWH3015175, BRAWH3017180, BRAWH3017259,
 35 BRAWH3019026, BRAWH3021724, BRAWH3022431, BRAWH3023415,
 BRAWH3024186, BRAWH3028796, BRAWH3029385, BRAWH3029806,

BRAWH3032571, BRAWH3033513, BRAWH3034668, BRAWH3034743,
BRAWH3037979, BRAWH3041556, BRAWH3043295, BRAWH3044122,
BRAWH3044985, BRAWH3046424, BRAWH3047692, BRAWH3048724,
BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402,
5 BRCAN2021325, BRCOC2001355, BRCOC2006164, BRHIP2029663,
BRHIP3001481, BRHIP3002000, BRHIP3002114, BRHIP3002141,
BRHIP3003063, BRHIP3003126, BRHIP3003795, BRHIP3004725,
BRHIP3005307, BRHIP3005673, BRHIP3007195, BRHIP3007223,
BRHIP3011082, BRHIP3012289, BRHIP3016032, BRHIP3019643,
10 BRHIP3021019, BRHIP3032374, BRHIP3033557, BRHIP3035006,
BRHIP3037543, BRHIP3038030, BRHIP3041587, BRSSN2004710,
BRSSN2011843, BRSTN2011961, BRSTN2016918, BRTHA2001304,
BRTHA2005448, BRTHA2026290, BRTHA2026311, BRTHA2027250,
BRTHA2030036, BRTHA2033683, BRTHA2035743, BRTHA2036295,
15 BRTHA2037247, BRTHA3003736, BRTHA3010135, BRTHA3014547,
BRTHA3021786, BRTHA3023403, BRTHA3026916, CHONS2002829,
COLON2004351, CTONG2010330, CTONG2020582, CTONG2026987,
FCBBF3001018, FCBBF3021191, FEBRA2013570, FEBRA2026582,
FEHRT2002708, FEKID2002637, HHDPC2008185, HSYRA2004550,
20 KIDNE2004531, KIDNE2010049, LYMPB2002236, NT2RI2004818,
NT2RI3001967, NT2RP7016508, NT2RP8003490, NT2RP8003787,
NT2RP8005546, OCBBF2000831, OCBBF2007039, OCBBF2024589,
OCBBF3001616, OCBBF3004487, OCBBF3021086, OCBBF3023175,
OCBBF3025503, OCBBF3026088, OCBBF3026361, PLACE5000492,
25 PLACE6003004, PLACE7003985, PLACE7004103, PLACE7004961,
PLACE7006090, PLACE7007379, PLACE7008136, PLACE7012111,
PLACE7014247, PLACE7016526, SKMUS2008585, SKMUS2009557,
SMINT2011406, SMINT2011509, SYNOV2017179, SYNOV4003174,
SYNOV4009139, T1ESE2000609, T1ESE2002665, TESTI2001364,
30 TESTI2005112, TESTI2007490, TESTI2018335, TESTI2021112,
TESTI2021654, TESTI2030901, TESTI2037877, TESTI2049062,
TESTI4000621, TESTI4002774, TESTI4002799, TESTI4003404,
TESTI4003565, TESTI4003602, TESTI4003703, TESTI4005399,
TESTI4007671, TESTI4010544, TESTI4010721, TESTI4012960,
35 TESTI4017854, TESTI4020342, TESTI4020596, TESTI4020819,
TESTI4021129, TESTI4021197, TESTI4023096, TESTI4024494,

TESTI4026080, TESTI4028182, TESTI4031066, TESTI4033177,
 TESTI4040598, TESTI4041482, TESTI4046073, TESTI4047808,
 TESTI4049786, TESTI4051424, TESTI4051865, TESTI4052219,
 THYMU3000390, THYMU3002825, THYMU3014372, THYMU3023400,
 5 THYMU3025683, THYMU3026306, THYMU3026479, THYMU3031878,
 THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428,
 THYMU3047115, THYMU3047891, TRACH2022113, TRACH2024730,
 TRACH3003037, TRACH3005274, TRACH3006800, TRACH3009008,
 TRACH3009061, TRACH3011313, TRACH3016455, TRACH3017409,
 10 TRACH3018108, TRACH3018261, TRACH3019621, TRACH3021544,
 TRACH3023516, TRACH3024020, TRACH3024081, TRACH3024342,
 TRACH3024512, TRACH3025316, TRACH3026303, TRACH3026650,
 TRACH3027229, TRACH3027701, TRACH3029329, TRACH3032150,
 TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042,
 15 UTERU3001946, UTERU3010604, UTERU3010919, UTERU3015299,
 UTERU3017441, UTERU3019708, UTERU3020090, UTERU3022168

The following seven clones are also predicted to belong to the category of enzyme and/or metabolism-related protein.

ADRGL2011190, BRAMY3008096, CTONG2002832, TESTI4052089,
 20 THYMU3024602, THYMU3044175, TRACH3021066

The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 13 clones.

BRACE3022303, BRAWH3017260, BRHIP2008756, BRHIP3028570,
 25 BRSTN2006638, NT2RI2004818, PLACE7009563, PLACE7016526,
 SMINT2014721, THYMU3025642, THYMU3033626, TRACH3029329,
 UTERU3010919

The following one clone is also predicted to belong to the category of cell division and/or cell proliferation-related protein.

30 TBAES2007481

The clones predicted to belong to the category of cytoskeleton-related protein are the following 51 clones.

BRACE2046976, BRACE3013874, BRACE3047482, BRACE3051819,
 35 BRAMY3015549, BRAWH3015175, BRAWH3018548, BRAWH3021580,
 BRAWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3032298,

BRAWH3049544, BRHIP3003340, BRHIP3012736, BRHIP3036936,
 BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA2031917,
 BRTHA3011361, BRTHA3025073, CTONG2008989, HSYRA2007338,
 LYMPB2002458, OCBBF3008835, OCBBF3027969, PEBLM2006298,
 5 PLACE7000266, PLACE7004103, PLACE7004961, SMINT2011406,
 SYNOV4003174, TESTI2006543, TESTI2034913, TESTI4001517,
 TESTI4005653, TESTI4008305, TESTI4041049, TESTI4051424,
 TESTI4051865, THYMU3020221, THYMU3038158, TLUNG2000654,
 TRACH3002890, TRACH3006379, TRACH3012460, TRACH3018524,
 10 TRACH3020769, TRACH3028837, UTERU3011837

The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 29 clones.

BRACE2016896, BRACE3032537, BRACE3034183, BRACE3039288,
 15 BRAWH3013264, BRAWH3032571, BRCOC2006164, BRHIP3004725,
 BRSSN2011843, BRTHA2026290, BRTHA3003736, BRTHA3014547,
 NT2RP7016508, NT2RP8005546, OCBBF3004487, OCBBF3021086,
 OCBBF3026361, PLACE5000492, TESTI4000621, TESTI4002799,
 TESTI4010721, TESTI4012960, THYMU3014372, THYMU3033626,
 20 THYMU3041428, TRACH3017409, TRACH3029462, UTERU3010919,
 UTERU3019708

The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 50 clones.

25 BRACE3033525, BRACE3041059, BRAMY4001652, BRAWH3010657,
 BRAWH3013264, BRAWH3034668, BRAWH3036247, BRAWH3037428,
 BRAWH3037979, BRCAN2000923, BRCAN2002892, BRCAN2006051,
 BRCAN2021325, BRCAN2021718, BRHIP2029663, BRHIP3002000,
 BRHIP3003126, BRHIP3007223, BRHIP3011082, BRSTN2010089,
 30 BRTHA2036295, BRTHA3012265, CHONS2002829, D9OST2004417,
 HHDP2008185, NETRP2003448, OCBBF2007039, OCBBF3021086,
 PLACE6003004, PLACE6010925, PLACE7006498, PLACE7007379,
 PLACE7012111, PLACE7016526, TESTI2023903, TESTI2036285,
 TESTI4003602, TESTI4012960, TESTI4014415, TESTI4030864,
 35 TESTI4051865, THYMU3036953, THYMU3047891, TRACH3004113,

TRACH3006800, TRACH3009061, TRACH3021544, TRACH3026650,
UTERU3001946, UTERU3012414

The following one clone is also predicted to belong to the category of protein synthesis and/or transport-related protein.

5 CTONG2002832

The clones predicted to belong to the category of cellular defense-related protein are the following four clones.

BRHIP3027191, SYNOV4009575, TESTI2023903, TRACH3029462

10 The clones predicted to belong to the category of development and/or differentiation-related protein are the following one clone.

CHONS2000797

The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 185 clones.

15 ASTRO2016114, BEAST2000981, BRACE2012625, BRACE2016896,
BRACE2019348, BRACE3019941, BRACE3025719, BRACE3026844,
BRACE3026947, BRACE3029021, BRACE3031743, BRACE3032537,
BRACE3034183, BRACE3039288, BRACE3040239, BRACE3041162,
BRACE3047482, BRACE3050270, BRALZ2013621, BRAMY2041347,
20 BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027,
BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209,
BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3011623,
BRAWH3013009, BRAWH3013264, BRAWH3015175, BRAWH3015610,
BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAWH3027533,
25 BRAWH3027607, BRAWH3027880, BRAWH3028796, BRAWH3031342,
BRAWH3031710, BRAWH3032571, BRAWH3035403, BRAWH3035936,
BRAWH3036247, BRAWH3036334, BRAWH3038055, BRAWH3042787,
BRAWH3044122, BRCAN2020331, BRCAN2021452, BRCOC2006164,
BRCOC2012386, BRHIP2027077, BRHIP2029663, BRHIP3002141,
30 BRHIP3004725, BRHIP3005037, BRHIP3007609, BRHIP3017256,
BRHIP3019824, BRHIP3027651, BRHIP3028246, BRHIP3039592,
BRSSN2011843, BRSTN2012069, BRTHA2026290, BRTHA2037247,
BRTHA3000456, BRTHA3003225, BRTHA3003736, BRTHA3010212,
BRTHA3014000, BRTHA3014547, BRTHA3028339, CHONS2000797,
35 CTONG2003517, CTONG2006235, CTONG2011801, CTONG2026987,
D9OST2003106, FCBBF3020030, FEBRA2002260, FEBRA2028457,

FEHRT2002708, HCASM2008154, KIDNE2018268, NETRP2003103,
NETRP2004017, NT2RI3009480, NT2RP7016508, NT2RP8005546,
NTONG2003805, NTONG2008483, OCBBF2014745, OCBBF2016928,
OCBBF3001333, OCBBF3001616, OCBBF3004487, OCBBF3008392,
5 OCBBF3019269, OCBBF3020263, OCBBF3021086, OCBBF3021361,
OCBBF3022827, OCBBF3025503, OCBBF3026361, PLACE5000492,
PLACE7004103, PLACE7005169, PLACE7007973, PLACE7008136,
PLACE7009757, PLACE7018512, PROST2002078, SMINT2011509,
SMINT2014721, SPLEN2012571, SPLEN2036608, TIESE2000609,
10 TIESE2000904, TESTI2036822, TESTI2040377, TESTI4000370,
TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796,
TESTI4003944, TESTI4005322, TESTI4005470, TESTI4012960,
TESTI4024494, TESTI4028182, TESTI4032913, TESTI4039904,
TESTI4051054, TESTI4052775, THYMU2008207, THYMU2038199,
15 THYMU3008105, THYMU3012983, THYMU3014372, THYMU3021586,
THYMU3022434, THYMU3023400, THYMU3026000, THYMU3030072,
THYMU3037617, THYMU3040829, THYMU3041428, THYMU3043200,
THYMU3045704, TKIDN2003396, TLIVE2001616, TLUNG2000654,
TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113,
20 TRACH3004412, TRACH3004424, TRACH3005274, TRACH3010079,
TRACH3010167, TRACH3015951, TRACH3017409, TRACH3021778,
TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750,
UTERU2037423, UTERU3012293, UTERU3015011, UTERU3016070,
UTERU3019708, UTERU3020090, UTERU3022168, UTERU3022588,
25 UTERU3023141

The following seven clones are also predicted to belong to the category of DNA-binding and/or RNA-binding protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI4002988,
TESTI4005500, TRACH1000193, TRACH3019290

30 The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 41 clones.

BRACE3042409, BRAWH2002333, BRAWH2014053, BRAWH3015175,
BRAWH3029385, BRAWH3029806, BRAWH3034743, BRAWH3037428,
BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2022126,
35 BRCOC2001355, BRCOC2006164, BRHIP3007195, BRSSN2004710,
BRTHA2026290, BRTHA2033683, BRTHA3026916, CTONG2020582,

HSYRA2004550, NETRP2003448, PLACE6019600, PLACE7004961,
 PLACE7006498, PLACE7016526, SMINT2011406, TESTI4010544,
 TESTI4014415, TESTI4028182, TESTI4029731, TESTI4040559,
 TESTI4041482, TESTI4052219, THYMU3013785, THYMU3047115,
 5 TRACH2024730, TRACH3024081, TRACH3029329, TRACH3031660,
 UTERU3012414

The following one clone is also predicted to belong to the category of ATP binding and/or GTP-binding protein.

ADRG2011190

10 The following 172 clones had hit data in Pfam (see Example 5), although it remains unclear as to which of the above-described categories each clone belongs. If data on polypeptides with a similar domain or motif can be accumulated, and their functions clarified in more detail, they may be
 15 classified into any of the above-described categories.

BLADE2001031, BRACE2010336, BRACE2013009, BRACE2017872,
 BRACE2023744, BRACE2034434, BRACE3001973, BRACE3002756,
 BRACE3005903, BRACE3014523, BRACE3019570, BRACE3022340,
 BRACE3026345, BRACE3036283, BRACE3040644, BRACE3043597,
 20 BRACE3046466, BRACE3048615, BRALZ2010842, BRAMY2031516,
 BRAMY2041384, BRAMY3002886, BRAMY3011501, BRAMY3015086,
 BRAMY3018754, BRAMY4000962, BRAWH2011796, BRAWH2016223,
 BRAWH3001783, BRAWH3003573, BRAWH3008167, BRAWH3011331,
 BRAWH3011577, BRAWH3014609, BRAWH3021574, BRAWH3022347,
 25 BRAWH3022719, BRAWH3024231, BRAWH3026938, BRAWH3027440,
 BRAWH3030772, BRAWH3030910, BRAWH3033448, BRAWH3034775,
 BRAWH3038252, BRAWH3038324, BRAWH3038827, BRAWH3042438,
 BRAWH3042568, BRAWH3044151, BRAWH3045118, BRAWH3048374,
 BRCAN2010665, BRCAN2019907, BRCAN2020234, BRCAN2025093,
 30 BRCOC2006639, BRHIP2013958, BRHIP2026346, BRHIP2027563,
 BRHIP3001878, BRHIP3004710, BRHIP3005142, BRHIP3005231,
 BRHIP3006449, BRHIP3007424, BRHIP3009753, BRHIP3010289,
 BRHIP3020733, BRHIP3029409, BRHIP3030230, BRHIP3033734,
 BRSSN2015497, BRTHA2038345, BRTHA3011187, BRTHA3021971,
 35 BRTHA3026161, BRTHA3027171, BRTHA3027638, CHONS2001287,
 CHONS2001834, DFNES2011221, ERLTF2002178, FCBBF3012443,

FCBBF3024911, FCBBF5000384, FEBRA2000805, FEBRA2023498,
 FEKID2002493, HCHON2009766, JCMLC2002751, KIDNE2015987,
 NT2RI3001573, NT2RI3005923, NT2RI3009524, NT2RP7007387,
 NT2RP7020343, NT2RP8000633, NT2RP8001604, NT2RP8006452,
 5 NT2RP8007920, NT2RP8009119, OCBBF3001202, OCBBF3005330,
 OCBBF3023913, OCBBF3026979, PEBLM2001803, PLACE6001933,
 PLACE7002303, PUAEN2000594, PUAEN2000684, SMINT2010753,
 SPLEN2022785, SPLEN2028417, SYNOV2003326, TBAES2003917,
 TBAES2007428, TESOP2002005, TESTI2005564, TESTI2009739,
 10 TESTI2011020, TESTI2018867, TESTI2049041, TESTI4001569,
 TESTI4002141, TESTI4002868, TESTI4004031, TESTI4007965,
 TESTI4011926, TESTI4013742, TESTI4024294, TESTI4035898,
 TESTI4039451, TESTI4041984, TESTI4043166, TESTI4046873,
 TESTI4047328, TESTI4047569, TESTI4051015, TESTI4052598,
 15 THYMU3003007, THYMU3012402, THYMU3015042, THYMU3015571,
 THYMU3017761, THYMU3019476, THYMU3021755, THYMU3033649,
 THYMU3040126, THYMU3046360, TKIDN2011051, TKIDN2011160,
 TLIVE2007736, TRACH3007689, TRACH3012106, TRACH3015346,
 TRACH3016805, TRACH3018606, TRACH3022296, TRACH3022758,
 20 TRACH3023203, TRACH3028855, TRACH3030855, TRACH3032570,
 UTERU2016669, UTERU3001394, UTERU3009775, UTERU3011558,
 UTERU3011579, UTERU3017995, UTERU3018255, UTERU3021850

Likewise, the following seven clones also had hit data in
 Pfam (see Example 5), although it remains unclear as to which of
 25 the above-described categories each clone belongs. When data on
 polypeptides with a similar domain or motif are accumulated, and
 their functions are clarified in more detail, these clones may
 also be classified into any of the above-described categories.

BRACE3026993// TSC-22/dip/bun family
 30 BRACE3046450// PDZ domain (Also known as DHR or GLGF). //PDZ
 domain (Also known as DHR or GLGF). //PDZ domain (Also known as
 DHR or GLGF). 1//PDZ domain (Also known as DHR or GLGF).
 CTONG2003764// Phorbol esters/diacylglycerol binding domain (C1
 domain)
 35 TBAES2004105// Thrombospondin type 1 domain
 TBAES2007379// EGF-like domain//EGF-like domain//Trypsin

Inhibitor like cysteine rich domain//EGF-like domain//EGF-like domain//Keratin, high sulfur B2 protein//EGF-like domain//EGF-like domain//Granulins//EGF-like domain//EGF-like domain//EGF-like domain

5 TBAES2008133// PDZ domain (Also known as DHR or GLGF).

UTERU2036507// Thrombospondin type 1 domain//NTR/C345C module

The function of a motif or domain may sometimes belong to more than one of the above-described functional categories, and there is also the possibility that such a motif or domain may be
 10 predicted to belong to every functional category. As new polypeptide data are accumulated and novel domains and motifs are found, a new functional domain or motif may be identified by re-analyzing deduced amino acid sequences in homology searches using updated databases. Thus in the future, the remaining
 15 clones, for which there are currently no hit data, may be classified into any of the above-described categories.

Since the polypeptides encoded by clones of the present invention contain full-length amino acid sequences, it is possible to analyze their biological activity and effect on
 20 cellular conditions such as cell proliferation and differentiation, by expressing the polypeptides as recombinant polypeptides using an appropriate expression system, injecting the recombinant into a cell, or raising a specific antibody against that polypeptide.

25 The biological activities of respective polypeptides can be analyzed by the methods as shown below.

Secretory protein, transmembrane protein:

"Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),

30 "Growth Factors" (Eds., I. McKay, I. Leigh, 1993),

"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The
 35 Practical Approach Series" (IRL PRESS),

"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F. Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

Signal transduction-related protein:

5 "Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),

"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or

10 "Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

Transcription-related protein:

"Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),

"Transcription Factors" (Ed., D. S. Latchman, 1993);

15 Enzyme and/or metabolism-related protein:

"Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS);

Cell division and/or cell proliferation-related protein:

20 "Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

25 "Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),

"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana Press) series;

Nuclear protein and/or RNA synthesis-related protein:

30 "Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),

"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

Protein synthesis and/or transport-related protein:

35 "Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS),

"Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

Cellular defense-related protein:

5 "DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,

"Chaperonin Protocols" (Eds., Schneider, Christine, 2000);
Development and/or differentiation-related protein:

10 "Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

15 "DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,

"RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

ATP- and/or GTP-binding protein:

20 "Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

When other techniques are used, the activity of a polypeptide can be analyzed according to the description in Methods in Enzymology (Academic Press).

25 In the above-described categorization, a clone predicted to belong to the secretory and/or membrane protein category refers to a clone having hit data in a homology search with some annotation to suggest that the clone encodes a secretory and/or membrane protein, such as a growth factor, cytokine, hormone, 30 signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, and connective tissue protein; or a clone in which the results of PSORT and SOSUI analyses for deduced ORF suggest the presence of a nucleotide 35 sequence encoding a signal sequence or transmembrane region; or a clone in which the results of a domain/motif search with Pfam

suggest the presence of domains/motifs that suggest receptors, ion channels, hormones, or growth factors, for example, seven-transmembrane receptors, pancreatic hormone peptides, ion transport proteins, or fibroblast growth factors.

5 A clone predicted to belong to the glycoprotein-related protein category means a clone having hit data in a homology search with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein; or a clone in which the results of a domain/motif search with Pfam
10 indicate the presence of domains and motifs such as a glycoprotein or glycosyltransferase that suggest the involvement of glycobiology, for example, immunoglobulin domain or glycosyl transferases group 1.

 A clone predicted to belong to the signal transduction-
15 related protein category means a clone having hit data in a homology search with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, and SH2 domain, suggesting that the clone encodes a signal transduction-related protein; or a clone in which the results of a
20 domain/motif search with Pfam suggest the presence of domains and motifs that suggest a protein kinase, dephosphoenzyme, SH2 domain, or small G protein, for example, eukaryotic protein kinase domain, protein phosphatase 2C, or Ras family.

 A clone predicted to belong to the transcription-related
25 protein category means a clone having hit data in a homology search with some annotation, such as transcription regulation, zinc finger, and homeobox, suggesting that the clone encodes a transcription-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of
30 domains and motifs that suggest a transcription factor or transcription-controlling protein, for example, bZIP transcription factor, Zinc finger, or C2H2 type.

 A clone predicted to belong to the category of disease-related protein means a clone having hit data in a homology
35 search with some annotation, such as disease mutation and syndrome, suggesting that the clone encodes a disease-related

protein; or a clone whose full-length nucleotide sequence has hit data in Swiss-Prot, nr, or RefSeq, where that hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), the human gene and disease database described later; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs, that suggest proteins with disease-specific expression or proteins involved in increasing or decreasing expression (depending on the disease), for example, Wilm's tumor protein or von Hippel-Lindau disease tumor suppressor protein.

A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data in a homology search with some annotation, such as metabolism, oxidoreductase, and E. C. No. (Enzyme commission number), suggesting that the clone encodes an enzyme and/or metabolism-related protein; or a clone in which the results of a domain/motif search with Pfam suggests the presence of domains and motifs that suggest transferase, synthase, or hydrolase, for example, aldehyde dehydrogenase family, chitin synthase, or glucose-6-phosphate dehydrogenase.

A clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data in a homology search with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, and apoptosis, suggesting that the clone encodes a cell division and/or cell proliferation-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest cyclin or cell proliferation-controlling protein, for example, cyclin or cell division protein.

A clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data in a homology search with some annotation, such as structural protein, cytoskeleton, actin-binding, and microtubules, suggesting that the clone encodes a cytoskeleton-related protein; or a clone in

which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest actin, kinesin, or fibronectin, for example, actin, fibronectin type I domain, or kinesin motor domain.

5 A clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data in a homology search with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, and polyadenylation, suggesting that the clone encodes a nuclear
10 protein and/or RNA synthesis-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest splicing factor, RNA synthase, or helicase, for example, hepatitis C virus RNA dependent RNA polymerase or DEAD/DEAH box helicase.

15 A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data in a homology search with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, and signal
20 recognition particle, suggesting that the clone encodes a protein synthesis and/or transport-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest translation-relating protein, ubiquitin-relating protein, or ribosomal
25 protein, for example, translation initiation factor SUI1, ubiquitin family, or ribosomal protein L16.

 A clone predicted to belong to the category of cellular defense-related protein means a clone having hit data in a homology search with some annotation, such as heat shock, DNA
30 repair, and DNA damage, suggesting that the clone encodes a cellular defense-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest chaperonin or DNA repair protein, for example, HSP90 protein or DNA mismatch repair
35 protein.

A clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data in a homology search with some annotation, such as developmental protein, suggesting that the clone encodes a development and/or differentiation-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest organogenesis-relating protein, for example, floricaula/leafy protein.

A clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having hit data in a homology search with some annotation, such as DNA-binding, RNA-binding, and such; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest DNA/RNA-relating enzyme group including transcription factor and DNA ligase or Zinc-finger relating protein, for example, transcription factor WhiB, B-box zinc finger, or tRNA synthetases class I (C).

A clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having hit data in a homology search with some annotation, such as ATP-binding, GTP-binding, and such; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest ATP/GTP-relating enzyme group including ATPase or G protein, for example, E1-E2 ATPase or Ras family.

It is possible to perform functional analysis of a protein involved in a disease as described above. It is also possible to analyze correlation between a protein's expression or activity and a certain disease by using a specific antibody obtained by using the expressed protein. Alternatively, it is possible to utilize the OMIM database, which is a database of human genes and diseases, to analyze the protein. New information is constantly being deposited into this database. Therefore, it is possible that one skilled in the art will find a new relationship between a particular disease and a gene of the present invention by using the most up-to-date database. Proteins involved in diseases are useful for developing

diagnostic markers or medicines for regulation of their expression and activity, or as gene therapy targets.

The proteins may have a variety of functions, including but not limited to the above 14 categories, such as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, or transcription-related proteins. When searching OMIM using these keywords, the proteins are revealed to be involved in a great number of diseases (the results of the OMIM search for secretory and membrane proteins are shown below as an Example). Associations between proteins related to signal transduction or transcription and diseases are reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). As another example and as described in "Biology of Cancer", many proteins are involved in cancers, including enzymes and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, (S. Matsubara, 1992) of Life Science series (Shokabo). As the above example clearly demonstrates, not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, and transcription-related proteins are often involved in diseases, and thus such proteins can be useful targets in the field of medical industry.

The results of the OMIM search for secretory and membrane proteins are shown below. The keywords used were:

- (1) secretion protein,
- (2) membrane protein,
- (3) channel, and
- (4) extracellular matrix.

Only the OMIM accession numbers are shown in the search results. The first 50 accession numbers displayed in the search

results are provided. Using this number, data showing the relationship between a disease and a gene or protein can be seen. OMIM data is renewed daily.

5 1) Secretion protein

When searching under these keywords, 436 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

10 *604667, *104760, *176860, *139320, *118910, *151675, *107400,
 *604029, #200100, *177061, *600946, *601693, *139250, *176880,
 *600998, *603850, *605083, *147572, *179513, *606055, *604028,
 *125950, *157147, *246700, *602926, *600560, *602421, *603215,
 185860, *600174, *179512, *109270, *179511, *179510, *179509,
 *601146, *604710, *177020, *138120, *170280, *600626, *164160,
 15 *168470, *154545, *603831, *601652, *104311, *601489, *603062,
 *102720

2) Membrane protein

20 When searching under these keywords, 1873 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

*130500, *605704, *305360, *153330, *109270, *173610, *170995,
 *120920, *170993, *309060, *104776, *602333, *605703, *602690,
 *605943, *159430, *600897, *606867, *133090, *601178, *602413,
 25 *602003, *604405, *605940, *603237, *109280, *606958, *600378,
 *606959, *602173, *107776, *602334, *125305, *602335, *309845,
 *601134, *605731, *606795, *185881, *607178, *603177, *154045,
 *603214, *603718, *606909, *600594, *603241, *606629, *603657,
 *600182

30

3) Channel (member of membrane proteins)

When searching under these keywords, 449 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

35 *176266, *600724, *605427, *182390, *123825, *114208, *114206,
 *114205, *176267, *600053, *601784, *603749, *182392, *600937,

*603415, *114204, *114209, *114207, *607370, *604528, *604527,
 *601011, *600760, *192500, *118425, *600228, *600359, *176261,
 *602235, *600761, *182389, *300008, *600877, *605692, *300338,
 *602232, *603537, *182391, *176263, *602343, *601328, *605874,
 5 *604385, *603939, *602208, *601534, *601958, *603220, *600504,
 *607368

4) Extracellular matrix

When searching under these keywords, 267 genes were
 10 registered as being associated with disease. The OMIM numbers
 for 50 of these genes are as follows.

*605912, *602201, *603479, *604633, *601418, *601548, *115437,
 *154870, *120361, *602285, *600754, *602262, *134797, *602261,
 *603320, *603321, *604871, *604629, *601807, #154700, *128239,
 15 *600310, *605470, *185250, *178990, *603767, *120360, *185261,
 *116935, *607056, *253700, *190180, *600985, *188826, *193300,
 *276901, *308700, *120150, *602109, *120324, *600514, #177170,
 #247100, #116920, #200610, *605127, *601313, *601652, *120180,
 *154790

20 In addition to these, various keywords shown in the above-
 mentioned categorizations or others can be used in an OMIM
 search to reveal involvement in disease.

Further, the use of nucleotide sequences of cDNAs of the
 present invention enables the expression frequency of genes
 25 corresponding to those cDNAs to be analyzed. Gene function can
 be predicted based on information obtained by expression
 frequency analysis.

There are several methods for analyzing the expression
 level of genes involved in disease. Differences in gene
 30 expression levels between diseased and normal tissues can be
 studied by analytical methods using, for example, Northern
 blotting, RT-PCR, DNA microarrays, etc. (Experimental Medicine,
 Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional
 volume) DNA Microarray and Advanced PCR Methods, Muramatsu &
 35 Nawa (eds.), Shujunsya (2000)). In addition to these analysis
 methods, computer analysis can be used to compare the nucleotide

sequences of expressed genes, and hence to analyze expression frequency. For example, in the "BODYMAP" database, gene clones are randomly extracted from cDNA libraries of various tissues and/or cells, clones homologous to each other are assigned to a
5 single cluster based on 3'-end nucleotide sequence homology information, genes are then classified into clusters, and the number of clones in each cluster is compared to gain information on expression frequency (<http://bodymap.ims.u-tokyo.ac.jp/>).

When these analytical methods result in observation of an
10 explicit difference between gene expression levels in diseased tissues and normal tissues, it can be concluded that the gene is closely involved in the disease or disorder. When gene expression is explicitly different between normal cells and cells reproducing specific disease-associated features, even if
15 they are not diseased tissues, it can be concluded that the gene is closely involved in a disease or disorder.

Of the 1,995 clones whose full-length nucleotide sequences were revealed, genes involved in a particular pathology or function were selected using the database shown below (see
20 Example 8; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains the nucleotide sequences of 1,402,069 clones, a sufficiently large population for analysis. Sequence information in the database was obtained by randomly selecting cDNA clones from
25 cDNA libraries derived from the various tissues and cells shown in Example 1, and determining the 5'-end sequences thereof.

The nucleotide sequence of each clone in this database was then categorized (clustered) based on nucleotide sequence homology determined with a search program. The number of clones
30 belonging to each cluster of each library was determined and normalized; and the ratio of a certain gene in a cDNA library was determined. This analysis provided information on the expression frequency of a gene in the tissue or cell that was the source of the cDNA library.

35 In order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in

tissues and cells, the libraries from the tissues or cells, which had been used in large-scale cDNA analyses, were taken as subjects for comparison of expression levels between different tissues or cells. Namely, expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which were derived the 600 or more cDNA clones whose nucleotide sequences had been analyzed. This analysis showed that the cDNA clones corresponded to the genes involved in the pathologies and functions indicated below. Each value in Tables 2 to 24 indicated below represents a relative expression frequency; a higher value indicates a higher expression level. Genes included in these Tables do not indicate such a big difference between compared libraries, but when compared with other tissue- or gene-derived libraries based on Example 9, they indicate a significant difference. Thus, these genes are specific to a tissue or cell, and can be considered useful diagnostic markers for disease, as well as useful for analyzing molecular mechanisms.

20 Osteoporosis-related genes

Osteoporosis is a pathology in which bones are easily broken owing to an overall decrease in bone components. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are thus genes involved in osteoporosis relevant to bone metabolism.

Nucleotide sequence-based analysis was carried out to identify genes whose expression frequencies were higher or lower in CD34+ cells (cells expressing glycoprotein CD34) treated with osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)), compared to untreated CD34+ cells, which are precursor cells in monocyte/macrophage lines. The result of comparative analysis of frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C), and from the RNA

of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) (Table 2), showed that the genes whose expression levels differed between the two were twelve clones indicated below.

5 BRAWH3018063, BRHIP3020046, BRSSN2013696, BRSTN2012069,
BRTHA2027229, D90ST2003106, D90ST2003989, D90ST2004417,
OCBBF2016928, TESTI4005653, TESTI4013474, THYMU3032798

These clones are involved in osteoporosis.

10 Genes involved in neural cell differentiation

Genes involved in neural cell differentiation are useful for treating neurological disease. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in
15 neurological disease.

A survey was performed for genes whose expression levels varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The
20 result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and cells subjected to differentiation treatment (NT2RP, NT2RI or NT2NE) (Table 3) showed that the genes whose expression levels differed between the two were 102 clones indicated below.

25 BLADE2004849, BRACE2003628, BRACE2012528, BRAMY2023939,
BRAMY2031516, BRAMY4002628, BRAWH3010461, BRAWH3017259,
BRAWH3018063, BRAWH3022651, BRAWH3024186, BRCAN2019653,
BRCAN2022126, BRCOC2012386, BRHIP3002000, BRHIP3007223,
BRHIP3021019, BRSTN2011961, BRSTN2012069, BRTHA2033155,
30 BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791,
BRTHA3021971, CHONS2002829, CTONG2006235, FCBBF3012443,
FEBRA2026582, LIVER2008465, NT2NE2011107, NT2NE2016041,
NT2RI2004818, NT2RI2009233, NT2RI2010795, NT2RI2015533,
NT2RI2023671, NT2RI2028537, NT2RI3001573, NT2RI3001967,
35 NT2RI3005861, NT2RI3005923, NT2RI3007095, NT2RI3008179,
NT2RI3009480, NT2RI3009524, NT2RP7003439, NT2RP7007387,

NT2RP7014178, NT2RP7014778, NT2RP7016508, NT2RP7017139,
 NT2RP7019682, NT2RP7020343, NT2RP8000633, NT2RP8001363,
 NT2RP8001407, NT2RP8001584, NT2RP8001604, NT2RP8001605,
 NT2RP8003490, NT2RP8003657, NT2RP8003787, NT2RP8005546,
 5 NT2RP8006452, NT2RP8006521, NT2RP8007416, NT2RP8007503,
 NT2RP8007920, NT2RP8008057, NT2RP8009119, NT2RP8009248,
 NTONG2008483, OCBBF2003518, OCBBF3001333, OCBBF3004908,
 PLACE7004103, PROST2017910, SMINT2009292, SPLEN2012571,
 T1ESE2000904, TESTI4002072, TESTI4002774, TESTI4002799,
 10 TESTI4005653, TESTI4007965, TESTI4012960, TESTI4018436,
 THYMU3001776, THYMU3002887, THYMU3029795, THYMU3041428,
 THYMU3047115, TRACH3003872, TRACH3004424, TRACH3006717,
 TRACH3007625, TRACH3009008, TRACH3016805, TRACH3016885,
 TRACH3026303, UTERU2016669

15 These genes are neurological disease-related genes.

Genes involved in Alzheimer's disease

Alzheimer's disease is a cranial neurological disease
 characterized by memory loss. As the disease advances, patients
 20 can no longer support themselves and require nursing.
 Alzheimer's disease eventually leads to brain atrophication.
 Environmental factors such as stress, and vascular factors such
 as hypertension and cholesterolemia, are assumed but not
 confirmed to contribute to the onset of Alzheimer's disease.
 25 Genes whose expression levels differ between normal brain
 tissues and tissues affected with Alzheimer's disease are
 expected to be involved in Alzheimer's disease. Such genes can
 be used to elucidate the disease's onset mechanism and in
 genetic diagnosis. cDNA libraries derived from the cerebral
 30 cortex of Alzheimer patients (BRALZ and BRASW) and a library
 derived from the whole tissues of a normal brain (BRAWH) were
 analyzed and compared (Table 4). Genes whose expression levels
 differed between the two were the 298 clones and five clones
 listed below.
 35 ASTRO2016114, BRACE2002392, BRACE2012528, BRACE3004371,
 BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031743,

BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863,
BRACE3042432, BRACE3045981, BRALZ2003119, BRALZ2007661,
BRALZ2008930, BRALZ2010842, BRALZ2011337, BRALZ2013621,
BRALZ2013690, BRALZ2014054, BRAMY2031516, BRAMY3002329,
5 BRAHY3004126, BRAHY3005912, BRAHY3008436, BRAWH2000256,
BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619,
BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054,
BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209,
BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562,
10 BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053,
BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244,
BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350,
BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896,
BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961,
15 BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726,
BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402,
BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907,
BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779,
BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508,
20 BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175,
BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715,
BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477,
BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548,
BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594,
25 BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884,
BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580,
BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347,
BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651,
BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168,
30 BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186,
BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989,
BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440,
BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616,
BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202,
35 BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796,
BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806,

BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054,
BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340,
BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448,
BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134,
5 BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890,
BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936,
BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334,
BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428,
BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230,
10 BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2019653,
BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153,
BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3003063,
BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409,
BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784,
15 BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSTN2010089,
BRSTN2012069, BRSTN2016992, BRTHA2033155, BRTHA3003736,
BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194,
BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971,
BRTHA3023403, CTONG2006235, CTONG2009033, CTONG2020582,
20 D9OST2003106, DFNES2001829, KIDNE2010049, MESAN2017133,
NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524,
NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483,
OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487,
PLACE7004103, PLACE7006240, PROST2007444, PROST2017910,
25 TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072,
TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210,
TESTI4005399, TESTI4005653, TESTI4006441, TESTI4013474,
TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887,
THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306,
30 THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827,
THYMU3038214, THYMU3041428, THYMU3044075, TRACH2013585,
TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424,
TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632,
TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885,
35 TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676,

TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399,
 UTERU3010409, UTERU3013167
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 TRACH1000193

5 These genes are involved in Alzheimer's disease.

Genes involved in Parkinson's disease

10 Parkinson's disease is a cranial neurological disease
 characterized by impaired production of the neurotransmitter
 dopamine in the substantia nigra in the brain. This results in
 dyskinesia, such as hand tremors, and impaired body movement due
 to muscular rigidity. Normally, the number of brain neurons
 gradually decreases with age. However, compared to healthy
 people, patients with Parkinson's disease experience a rapid and
 15 marked decrease in the number of neurons in their substantia
 nigra. Genes whose expression levels differ between tissues of
 the whole brain and the nigra are expected to be involved in
 Parkinson's disease. These genes exhibit nigra-specific
 alterations in their expression levels, and can be used to
 20 elucidate the disease onset mechanism and in gene diagnosis.
 cDNA libraries derived from the substantia nigra (BRSSN) and a
 library derived from whole tissues of a normal brain (BRAWH)
 were analyzed and compared (Table 5). Genes whose expression
 levels differed between the two were the 305 clones and five
 25 clones listed below.

ASTRO2016114, BRACE2012528, BRACE2017844, BRACE3004371,
 BRACE3004767, BRACE3022340, BRACE3025719, BRACE3026802,
 BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631,
 BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981,
 30 BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912,
 BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078,
 BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812,
 BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,
 BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305,
 35 BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,
 BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,

BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975,
BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886,
BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559,
BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602,
5 BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101,
BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005,
BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,
BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639,
10 BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825,
BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063,
BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200,
15 BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012,
BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459,
BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274,
20 BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242,
BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574,
BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461,
25 BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385,
BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
30 BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743,
BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247,
BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979,
35 BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324,
BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386,

BRHIP2015153, BRHIP2027077, BRHIP2029643, BRHIP3001573,
 BRHIP3002000, BRHIP3003063, BRHIP3003984, BRHIP3004774,
 BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675,
 BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019,
 5 BRHIP3028246, BRHIP3028570, BRSSN2004303, BRSSN2004710,
 BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198,
 BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2010089,
 BRSTN2011961, BRSTN2012069, BRSTN2016992, BRSTN2017104,
 BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135,
 10 BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791,
 BRTHA3020771, BRTHA3021971, BRTHA3023403, CTONG2006235,
 CTONG2009033, CTONG2011801, CTONG2020582, D9OST2003106,
 DFNES2001829, KIDNE2010049, MESAN2017133, NT2RI2009233,
 NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
 15 NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518,
 OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103,
 PLACE7006240, PROST2007444, SMINT2009292, T1ESE2000904,
 TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072,
 TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210,
 20 TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908,
 TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350,
 THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
 THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214,
 THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037,
 25 TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,
 TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079,
 TRACH3016805, TRACH3016885, TRACH3022198, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,
 TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
 30 UTERU3013167
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 TRACH1000193

These genes are involved in Parkinson's disease.

35 Genes involved in short-term memory and dementia

In the brain, the hippocampus is a highly important memory-related area. The hippocampus functions to establish a memory by judging whether acquired information is necessary, and then accumulating the memory in another area of the brain. According to clinical findings, patients can retain a new memory for only about five minutes with an abnormal, or at worst without a hippocampus. Some dementia patients are presumed to have hippocampus abnormalities. Thus, genes whose expression levels differ between tissues of the whole brain and the hippocampus are expected to be involved in memory or dementia. Such genes can be used to elucidate the mechanism underlying memory, and in gene diagnosis. cDNA libraries derived from the hippocampus (BRHIP) and from the whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 6). Genes whose expression levels differed between the two were the 438 clones and five clones listed below.

ASTRO2016114, BRACE2002392, BRACE2012528, BRACE2017359,
 BRACE2017397, BRACE2017844, BRACE3004046, BRACE3004371,
 BRACE3004767, BRACE3009416, BRACE3022340, BRACE3027931,
 BRACE3029021, BRACE3031185, BRACE3031743, BRACE3032385,
 BRACE3032631, BRACE3036156, BRACE3039358, BRACE3040863,
 BRACE3042326, BRACE3042432, BRACE3045078, BRACE3045981,
 BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005184,
 BRAMY3005912, BRAMY3007078, BRAMY3008436, BRAMY4000915,
 BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364,
 BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958,
 BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053,
 BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514,
 BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884,
 BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833,
 BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335,
 BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892,
 BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867,
 BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657,
 BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331,
 BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685,

BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662,
BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264,
BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017,
BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123,
5 BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260,
BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369,
BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529,
BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318,
BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574,
10 BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724,
BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542,
BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156,
BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421,
BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506,
15 BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420,
BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607,
BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880,
BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754,
BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538,
20 BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910,
BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298,
BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293,
BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114,
BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775,
25 BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914,
BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270,
BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394,
BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055,
BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665,
30 BRCAN2019953, BRCAN2022126, BRCAN2025093, BRCOC2012386,
BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177,
BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125,
BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735,
BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563,
35 BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626,
BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338,

BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878,
 BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141,
 BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931,
 BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340,
 5 BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845,
 BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710,
 BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037,
 BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673,
 BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294,
 10 BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172,
 BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409,
 BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082,
 BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753,
 BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269,
 15 BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185,
 BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997,
 BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675,
 BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109,
 BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855,
 20 BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880,
 BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733,
 BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656,
 BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795,
 BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160,
 25 BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246,
 BRHIP3028570, BRHIP3028742, BRSTN2010089, BRSTN2012069,
 BRSTN2016992, BRTHA2001953, BRTHA2008502, BRTHA2031517,
 BRTHA2033155, BRTHA2035743, BRTHA3003417, BRTHA3003736,
 BRTHA3005988, BRTHA3007662, BRTHA3010135, BRTHA3010212,
 30 BRTHA3011194, BRTHA3011265, BRTHA3012265, BRTHA3017791,
 BRTHA3020771, BRTHA3021971, BRTHA3023403, CHONS2002829,
 CTONG2006235, CTONG2009033, CTONG2020582, D9OST2003106,
 DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133,
 NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
 35 NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920,
 NTONG2008483, OCBBF2000831, OCBBF2003518, OCBBF2018618,

OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240,
 PROST2007444, SMINT2012179, SYNOV4004210, TBAES2007428,
 TESTI2005112, TESTI2005564, TESTI2021654, TESTI4001569,
 TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602,
 5 TESTI4003703, TESTI4003944, TESTI4004210, TESTI4005399,
 TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158,
 TESTI4029297, THYMU3000776, THYMU3002887, THYMU3003007,
 THYMU3003350, THYMU3007308, THYMU3008105, THYMU3021586,
 THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798,
 10 THYMU3032867, THYMU3034671, THYMU3037827, THYMU3038214,
 THYMU3044075, TKIDN2000319, TRACH2013585, TRACH3002752,
 TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717,
 TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008,
 TRACH3010079, TRACH3016805, TRACH3016885, TRACH3022198,
 15 TRACH3024342, TRACH3024671, TRACH3025316, TRACH3026303,
 TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932,
 TRACH3038399, TSTOM2000235, UTERU3005422, UTERU3010409,
 UTERU3013167, UTERU3016273
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 20 TRACH1000193

These genes are involved in memory and dementia.

Genes involved in equilibrium sense and movement function

The cerebellum is the center of equilibrium sense, muscular
 25 movement, and motor learning. This area is thought to be
 involved in motor control, and smooth movements are achieved
 unconsciously due to cerebellum action. Recent studies have
 elucidated that the cerebellum participates in not only simple
 movements but also in establishing higher-order movements such
 30 as reading and writing. Thus, genes whose expression levels
 differ between tissues of the whole brain and the cerebellum are
 expected to be involved in equilibrium sense or motor function,
 which can be useful for elucidating the molecular mechanism
 controlled by the brain. cDNA libraries derived from the
 35 cerebellum (BRACE) and from the whole tissues of a normal brain
 (BRAWH) were analyzed and compared (Table 7). Genes whose

expression levels differed between the two were the 502 clones and nine clones listed below.

ASTRO2016114, BRACE1000475, BRACE2002392, BRACE2003628,
 BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625,
 5 BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947,
 BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896,
 BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844,
 BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633,
 BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312,
 10 BRACE2027382, BRACE2028956, BRACE2030039, BRACE2032584,
 BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191,
 BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976,
 BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973,
 BRACE3002344, BRACE3002541, BRACE3002756, BRACE3003866,
 15 BRACE3004046, BRACE3004371, BRACE3004767, BRACE3004887,
 BRACE3004981, BRACE3005870, BRACE3005903, BRACE3006553,
 BRACE3007649, BRACE3007869, BRACE3009075, BRACE3009265,
 BRACE3009392, BRACE3009416, BRACE3009539, BRACE3010702,
 BRACE3011447, BRACE3011774, BRACE3013418, BRACE3013874,
 20 BRACE3013986, BRACE3014523, BRACE3014714, BRACE3015090,
 BRACE3015898, BRACE3016020, BRACE3016167, BRACE3016580,
 BRACE3016788, BRACE3016810, BRACE3016862, BRACE3017253,
 BRACE3018083, BRACE3019570, BRACE3019611, BRACE3019817,
 BRACE3019941, BRACE3020356, BRACE3020669, BRACE3021430,
 25 BRACE3021517, BRACE3021805, BRACE3022051, BRACE3022303,
 BRACE3022312, BRACE3022340, BRACE3022847, BRACE3023604,
 BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024537,
 BRACE3024879, BRACE3025627, BRACE3025719, BRACE3026161,
 BRACE3026290, BRACE3026345, BRACE3026456, BRACE3026802,
 30 BRACE3026844, BRACE3026947, BRACE3027256, BRACE3027931,
 BRACE3028360, BRACE3028895, BRACE3028998, BRACE3029005,
 BRACE3029021, BRACE3029205, BRACE3029447, BRACE3030538,
 BRACE3031161, BRACE3031184, BRACE3031185, BRACE3031315,
 BRACE3031372, BRACE3031579, BRACE3031728, BRACE3031743,
 35 BRACE3031843, BRACE3032385, BRACE3032537, BRACE3032538,
 BRACE3032631, BRACE3032980, BRACE3033525, BRACE3034183,

BRACE3034389, BRACE3034964, BRACE3034993, BRACE3035168,
BRACE3036156, BRACE3036271, BRACE3036283, BRACE3037612,
BRACE3037637, BRACE3037803, BRACE3038012, BRACE3038030,
BRACE3038570, BRACE3038760, BRACE3039288, BRACE3039358,
5 BRACE3039378, BRACE3039454, BRACE3040012, BRACE3040239,
BRACE3040504, BRACE3040644, BRACE3040863, BRACE3041059,
BRACE3041162, BRACE3041827, BRACE3042046, BRACE3042210,
BRACE3042326, BRACE3042409, BRACE3042432, BRACE3042594,
BRACE3043597, BRACE3044090, BRACE3044172, BRACE3044247,
10 BRACE3044377, BRACE3044495, BRACE3045078, BRACE3045145,
BRACE3045424, BRACE3045708, BRACE3045981, BRACE3046049,
BRACE3046152, BRACE3046294, BRACE3046466, BRACE3046491,
BRACE3046609, BRACE3046837, BRACE3046855, BRACE3046966,
BRACE3047018, BRACE3047482, BRACE3047801, BRAMY2031516,
15 BRAMY3002329, BRAMY3004126, BRAMY3004364, BRAMY3005912,
BRAMY3008436, BRAMY3009491, BRAWH2000256, BRAWH2002333,
BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796,
BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866,
BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223,
20 BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785,
BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638,
BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573,
BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037,
BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167,
25 BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461,
BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833,
BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577,
BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929,
BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009,
30 BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609,
BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610,
BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180,
BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980,
BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969,
35 BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820,
BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928,

BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641,
 BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431,
 BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719,
 BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172,
 5 BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231,
 BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349,
 BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533,
 BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675,
 BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223,
 10 BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313,
 BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772,
 BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342,
 BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571,
 BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513,
 15 BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668,
 BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403,
 BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077,
 BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561,
 BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533,
 20 BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252,
 BRAWH3038324, BRCAN2010665, BRCAN2019953, BRCAN2022126,
 BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077,
 BRHIP2029643, BRHIP3001360, BRHIP3001573, BRHIP3002000,
 BRHIP3002114, BRHIP3003063, BRHIP3003126, BRHIP3003961,
 25 BRHIP3003984, BRHIP3004215, BRHIP3004774, BRHIP3005801,
 BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675,
 BRHIP3017855, BRHIP3018784, BRHIP3021019, BRHIP3028246,
 BRHIP3028570, BRSSN2011843, BRSSN2013696, BRSTN2010089,
 BRSTN2011961, BRSTN2012069, BRSTN2016992, BRTHA2033155,
 30 BRTHA2035743, BRTHA3003736, BRTHA3005988, BRTHA3009858,
 BRTHA3010135, BRTHA3010212, BRTHA3010530, BRTHA3011194,
 BRTHA3011265, BRTHA3011998, BRTHA3017791, BRTHA3020771,
 BRTHA3021708, BRTHA3021971, BRTHA3023403, CHONS2002829,
 CTONG2006235, CTONG2009033, CTONG2020582, CTONG2027959,
 35 D9OST2003106, DFNES2001829, KIDNE2010049, KIDNE2017153,
 LIVER2008465, MESAN2017133, NOVAR2000783, NT2RI2009233,

NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
 NT2RP8001605, NT2RP8007920, NT2RP8009119, NTONG2008483,
 NTONG2009468, OCBBF2003518, OCBBF2014745, OCBBF2018618,
 OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240,
 5 PROST2007444, TBAES2007428, TESTI2005112, TESTI2018867,
 TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799,
 TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005013,
 TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908,
 TESTI4022158, TESTI4029297, TESTI4032913, TESTI4043223,
 10 THYMU3000776, THYMU3002887, THYMU3003350, THYMU3007308,
 THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
 THYMU3032798, THYMU3032867, THYMU3033626, THYMU3034671,
 THYMU3037827, THYMU3038214, THYMU3044075, TLIVE2007736,
 TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872,
 15 TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689,
 TRACH3007995, TRACH3008632, TRACH3009008, TRACH3010079,
 TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671,
 TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570,
 TRACH3036932, TRACH3038399, UTERU3000670, UTERU3010409,
 20 UTERU3013167, UTERU3015011
 BRACE3002184, BRACE3026993, BRACE3046450, BRAMY3008096,
 BRAWH3013197, BRAWH3028645, BRTHA3004432, TESTI4002988,
 TRACH1000193

These genes are involved in equilibrium sense or motor
 25 function.

Genes involved in signaling from sensory organs

The thalamus is an area which comprises many neurons
 strongly connected to the cerebrum, and which transmits sensory
 30 information from the spinal cord or such to the responsible area
 of the cerebrum. The thalamus also controls the direction of
 movement from the cerebrum. For example, the thalamus resolves
 vision into the elements of size, shape, and color, and resolves
 sound into volume and sweetness or harshness to the ear, and
 35 then transmits this information to the sensory area of the
 cerebral cortex. Thus, genes whose expression levels differ

between tissues of the whole brain and the thalamus are expected to be involved in signaling from sensory organs. These genes can be used to elucidate the molecular mechanism underlying signaling controlled by the brain. cDNA libraries derived from the thalamus (BRTHA) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 8). Genes whose expression levels differed between the two were the 440 clones and eight clones listed below.

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE2002392,
 10 BRACE2012528, BRACE2019348, BRACE3004371, BRACE3004767,
 BRACE3019941, BRACE3022312, BRACE3022340, BRACE3031185,
 BRACE3031743, BRACE3032385, BRACE3032631, BRACE3036156,
 BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981,
 BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912,
 15 BRAMY3008436, BRAMY3009556, BRAMY3010654, BRAMY4001863,
 BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364,
 BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958,
 BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053,
 BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514,
 20 BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884,
 BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833,
 BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335,
 BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892,
 BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867,
 25 BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657,
 BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331,
 BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685,
 BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662,
 BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264,
 30 BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017,
 BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123,
 BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260,
 BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369,
 BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529,
 35 BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318,
 BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574,

BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724,
BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542,
BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156,
BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421,
5 BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506,
BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420,
BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607,
BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880,
BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754,
10 BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538,
BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910,
BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298,
BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293,
BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114,
15 BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775,
BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914,
BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270,
BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394,
BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055,
20 BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2002892,
BRCAN2010665, BRCAN2020234, BRCAN2022126, BRCAN2025093,
BRCOC2006164, BRCOC2012386, BRHIP2013958, BRHIP2015153,
BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3002691,
BRHIP3002920, BRHIP3003063, BRHIP3003961, BRHIP3003984,
25 BRHIP3004215, BRHIP3004774, BRHIP3007223, BRHIP3007409,
BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784,
BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570,
BRSSN2015497, BRSTN2010089, BRSTN2011961, BRSTN2012069,
BRSTN2016992, BRTHA2000969, BRTHA2001304, BRTHA2001953,
30 BRTHA2002091, BRTHA2003759, BRTHA2005448, BRTHA2006720,
BRTHA2008502, BRTHA2008598, BRTHA2010672, BRTHA2012189,
BRTHA2014647, BRTHA2018304, BRTHA2019726, BRTHA2019743,
BRTHA2020400, BRTHA2020566, BRTHA2020642, BRTHA2020695,
BRTHA2020721, BRTHA2020781, BRTHA2020910, BRTHA2021212,
35 BRTHA2021440, BRTHA2021450, BRTHA2022074, BRTHA2022914,
BRTHA2022968, BRTHA2023402, BRTHA2023437, BRTHA2024177,

BRTHA2024354, BRTHA2024712, BRTHA2025869, BRTHA2026071,
 BRTHA2026290, BRTHA2026311, BRTHA2027227, BRTHA2027229,
 BRTHA2027250, BRTHA2028297, BRTHA2029969, BRTHA2030036,
 BRTHA2030213, BRTHA2031517, BRTHA2031917, BRTHA2032763,
 5 BRTHA2033122, BRTHA2033155, BRTHA2033320, BRTHA2033469,
 BRTHA2033683, BRTHA2034281, BRTHA2034576, BRTHA2035743,
 BRTHA2036055, BRTHA2036295, BRTHA2037247, BRTHA2038279,
 BRTHA2038345, BRTHA2038353, BRTHA3000456, BRTHA3002411,
 BRTHA3003225, BRTHA3003417, BRTHA3003736, BRTHA3005988,
 10 BRTHA3006593, BRTHA3007469, BRTHA3007662, BRTHA3009858,
 BRTHA3010135, BRTHA3010212, BRTHA3010469, BRTHA3010530,
 BRTHA3010540, BRTHA3010717, BRTHA3011187, BRTHA3011194,
 BRTHA3011229, BRTHA3011265, BRTHA3011306, BRTHA3011361,
 BRTHA3011510, BRTHA3011892, BRTHA3011998, BRTHA3012265,
 15 BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3014105,
 BRTHA3014507, BRTHA3014547, BRTHA3014835, BRTHA3014854,
 BRTHA3014920, BRTHA3016616, BRTHA3017791, BRTHA3018409,
 BRTHA3018623, BRTHA3019183, BRTHA3020369, BRTHA3020771,
 BRTHA3021569, BRTHA3021708, BRTHA3021786, BRTHA3021971,
 20 BRTHA3022641, BRTHA3023403, BRTHA3023590, BRTHA3023929,
 BRTHA3024600, BRTHA3025073, BRTHA3026161, BRTHA3026180,
 BRTHA3026556, BRTHA3026916, BRTHA3027171, BRTHA3027318,
 BRTHA3027638, BRTHA3027820, BRTHA3027879, BRTHA3027957,
 BRTHA3028339, BRTHA3028505, CHONS2002829, CTONG2006235,
 25 CTONG2009033, CTONG2011801, CTONG2020582, D9OST2003106,
 DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133,
 NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
 NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920,
 NTONG2008483, OCBBF2003518, OCBBF2009536, OCBBF2018618,
 30 OCBBF3001333, OCBBF3004487, OCBBF3008835, PLACE6003004,
 PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292,
 TBAES2007428, TESTI2005112, TESTI2021654, TESTI2039342,
 TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602,
 TESTI4003703, TESTI4004210, TESTI4004695, TESTI4005399,
 35 TESTI4005653, TESTI4006441, TESTI4007965, TESTI4010979,
 TESTI4013474, TESTI4014908, TESTI4022158, TESTI4029297,

TESTI4032913, THYMU3000776, THYMU3002887, THYMU3003350,
 THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
 THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214,
 THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037,
 5 TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,
 TRACH3007689, TRACH3008508, TRACH3008632, TRACH3009008,
 TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,
 TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
 10 UTERU3012414, UTERU3013167, UTERU3017995, UTERU3018172
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 BRTHA3024233, CTONG2002832, THYMU3046350, TRACH1000193

These genes are involved in signaling from sensory organs.

15 Genes involved in emotional reaction

The amygdala is the center of emotion in the brain. Information passing through the amygdala induces an emotional reaction, for example, panic or fear. When a strong fear reaction is produced due to the emotional evaluation of stimulus
 20 in the amygdala, the amygdala transmits an alert signal to each area of the brain. This results in various reactions such as sweating palms, palpitation, elevated blood pressure, and rapid secretion of adrenaline. In other words, the amygdala transmits signals which cause the body to be on the alert and is a tissue
 25 involved in a kind of defense instinct. Thus, genes whose expression levels differ between tissues of the whole brain and the amygdala are expected to be involved in emotional reaction. Such genes can be used to elucidate the molecular mechanism underlying emotional reaction, fear, or panic. cDNA libraries
 30 derived from the amygdale (BRAMY) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 9). Genes whose expression levels differed between the two were the 357 clones and nine clones listed below.

ASTRO2016114, BRACE2002392, BRACE2012528, BRACE2017397,
 35 BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340,
 BRACE3031185, BRACE3031315, BRACE3031743, BRACE3032385,

BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432,
BRACE3045981, BRAMY2015516, BRAMY2021098, BRAMY2022320,
BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895,
BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609,
5 BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384,
BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537,
BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508,
BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184,
BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449,
10 BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491,
BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603,
BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234,
BRAMY4001652, BRAMY4001863, BRAMY4001913, BRAMY4002575,
BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078,
15 BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812,
BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,
BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305,
BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,
BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,
20 BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975,
BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886,
BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559,
BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602,
BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101,
25 BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005,
BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,
BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639,
BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825,
30 BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063,
BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200,
BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012,
35 BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459,

BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274,
BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242,
BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
5 BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574,
BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461,
BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385,
BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
10 BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743,
BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
15 BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247,
BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979,
BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324,
BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386,
20 BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3002000,
BRHIP3002691, BRHIP3003063, BRHIP3003984, BRHIP3004215,
BRHIP3004774, BRHIP3005673, BRHIP3007223, BRHIP3007409,
BRHIP3008320, BRHIP3012736, BRHIP3014675, BRHIP3017146,
BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019,
25 BRHIP3028246, BRHIP3028570, BRSTN2010089, BRSTN2012069,
BRSTN2016992, BRTHA2026071, BRTHA2033155, BRTHA3003736,
BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194,
BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971,
BRTHA3023403, BRTHA3026916, CHONS2002829, CTONG2006235,
30 CTONG2009033, CTONG2020582, D9OST2003106, DFNES2001829,
KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2010795,
NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2000831,
OCBBF2003518, OCBBF2018618, OCBBF2030927, OCBBF3001333,
35 OCBBF3004487, OCBBF3009244, PLACE6008315, PLACE6010936,
PLACE7004103, PLACE7006240, PROST2007444, SPLEN2012571,

SYNOV4004210, SYNOV4009575, TBAES2007428, TESTI2005112,
 TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799,
 TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005399,
 TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158,
 5 TESTI4029297, TESTI4032913, TESTI4043223, TESTI4046073,
 THYMU3000776, THYMU3002887, THYMU3003350, THYMU3008105,
 THYMU3019476, THYMU3021586, THYMU3026000, THYMU3026306,
 THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827,
 THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752,
 10 TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717,
 TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008,
 TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,
 TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
 15 UTERU3013167
 BRACE3046450, BRAMY3008096, BRAWH3013197, BRAWH3028645,
 BRTHA3004432, TESTI4002988, THYMU3046350, TRACH1000193,
 TRACH3019290

These genes are involved in emotional reaction.

20

Cancer-related genes

Cancer tissues are assumed to express a distinct set of
 genes distinct from normal tissues, and thus expression of these
 genes can contribute to carcinogenesis in tissues and cells.
 25 Thus, genes whose expression patterns in cancer tissues differ
 from those in normal tissues are cancer-related genes. A search
 was carried out for genes whose expression levels in cancer
 tissues differed from those in normal tissues.

The result of comparative analysis of cDNA libraries
 30 derived from breast tumor (TBAES) and normal breast (BEAST)
 (Table 10) showed that the genes whose expression levels
 differed between the two were the ten and four clones listed
 below.

BRSTN2011961, BRSTN2012069, TBAES2003917, TBAES2005361,
 35 TBAES2007428, TBAES2007548, TBAES2007862, TESTI2005564,
 TESTI4017854, TRACH3016805

TBAES2004105, TBAES2007379, TBAES2007481, TBAES2008133

The result of comparative analysis of cDNA libraries derived from cervical tumor (TCERX) and normal cervical duct (CERVX) (Table 11) showed that the genes whose expression levels

5 differed between the two were six clones listed below.

BRACE2017397, BRHIP2027077, BRSTN2011961, BRSTN2012069,
CERVX2000812, CERVX2000968

The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) (Table

10 12) showed that the genes whose expression levels differed between the two were ten clones listed below.

BRSTN2011961, BRSTN2012069, COLON2001829, COLON2001866,
COLON2004351, COLON2004911, COLON2005623, COLON2005735,
OCBBF3001333, SMINT2017964

The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) (Table 13) showed that the genes whose expression levels

15 differed between the two were the 14 clones listed below.

BRAMY3004364, BRAWH3027533, BRHIP3007223, BRSTN2011961,
20 BRSTN2012069, CTONG2011801, CTONG3002518, SMINT2009292,
TESOP2002005, TESOP2003308, TESOP2004110, TESOP2008556,
UTERU3015011, UTERU3017995

The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE)

25 (Table 14) showed that the genes whose expression levels differed between the two were the 43 clones listed below.

BRACE2002392, BRACE2012528, BRACE3004371, BRAMY2039630,
BRAMY3004364, BRAMY3008436, BRAWH2004078, BRAWH3012662,
BRAWH3021574, BRAWH3022651, BRAWH3037428, BRCAN2019953,
30 BRCAN2022126, BRHIP3002000, BRHIP3002691, BRHIP3012997,
BRHIP3020046, BRSTN2012069, BRSTN2016992, BRTHA3010212,
CTONG2006235, KIDNE2004531, KIDNE2010049, KIDNE2014496,
KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268,
NT2RI2015533, NT2RP7007387, OCBBF3004487, PLACE6008315,
35 SYNOV4004210, TESTI2005112, THYMU3001776, THYMU3002887,

THYMU3029795, THYMU3032867, TKIDN2000319, TKIDN2003396,
TKIDN2010602, TKIDN2011051, TKIDN2011160

The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) (Table 5 15) showed that the genes whose expression levels differed between the two were the 14 and two clones listed below.

BRAWH3022651, BRCAN2020412, BRSTN2012069, BRTHA3003736,
CTONG2006235, LIVER2008465, TESTI4013474, THYMU3002887,
THYMU3038158, TLIVE2000142, TLIVE2001616, TLIVE2007736,
10 TLIVE2008797, TRACH3027229
THYMU3046350, TLIVE2007192

The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) (Table 16) showed that the genes whose expression levels differed 15 between the two were the 17 clones listed below.

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069,
HLUNG2012600, MESAN2009156, NTONG2008483, PROST2007444,
TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297,
THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428,
20 TRACH3022198

The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table 17A) showed the genes whose expression levels differed between the two were the three clones listed below.

25 BRSTN2012069, NOVAR2000783, THYMU3002887

The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) (Table 18) showed that the genes whose expression levels differed between the two were the nine clones listed below.

30 BRSTN2012069, CHONS2002829, STOMA2003894, STOMA2004663,
THYMU3001776, TSTOM2000235, TSTOM2001571, TSTOM2002611,
TSTOM2002682

The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) 35 (Table 19) showed that the genes whose expression levels

differed between the two were the 128 and three clones listed below.

BRACE2012528, BRACE2017397, BRACE3004371, BRACE3036283,
 BRACE3040863, BRAMY2031516, BRAMY3005184, BRAWH2004078,
 5 BRAWH3004350, BRAWH3022651, BRAWH3024186, BRAWH3029806,
 BRAWH3031342, BRCAN2022126, BRHIP3001076, BRHIP3002000,
 BRHIP3002141, BRHIP3005307, BRHIP3007223, BRHIP3017855,
 BRHIP3020046, BRSTN2010089, BRSTN2011961, BRSTN2012069,
 BRSTN2016892, BRTHA3003736, BRTHA3011265, BRTHA3023403,
 10 BRTHA3027879, CHONS2002829, CTONG2001932, CTONG2003517,
 CTONG2006235, CTONG2011801, CTONG3002518, DFNES2001829,
 KIDNE2010049, LIVER2008465, NT2RI3005923, OCBBF3001333,
 OCBBF3004487, PLACE6008315, PLACE7006240, PROST2007444,
 SPLEN2012571, SYNOV4000598, SYNOV4009575, T1ESE2000904,
 15 TESTI4002072, TESTI4002195, TESTI4002774, TESTI4002799,
 TESTI4003703, TESTI4003944, TESTI4005399, TESTI4005653,
 TESTI4024245, TESTI4029297, THYMU3002887, THYMU3021586,
 THYMU3026350, THYMU3032798, THYMU3034616, THYMU3034671,
 TRACH3003872, TRACH3005699, TRACH3006800, TRACH3008632,
 20 TRACH3009008, TUTER1000014, TUTER2001433, UTERU2000300,
 UTERU2014998, UTERU2016464, UTERU2016669, UTERU2020226,
 UTERU2022955, UTERU2023941, UTERU2024042, UTERU2027369,
 UTERU2028377, UTERU2029660, UTERU2035926, UTERU2037423,
 UTERU3000670, UTERU3001029, UTERU3001394, UTERU3001946,
 25 UTERU3004635, UTERU3005264, UTERU3005422, UTERU3006538,
 UTERU3006720, UTERU3007108, UTERU3009775, UTERU3010029,
 UTERU3010409, UTERU3010604, UTERU3010892, UTERU3010919,
 UTERU3011092, UTERU3011398, UTERU3011558, UTERU3011579,
 UTERU3011837, UTERU3012293, UTERU3012414, UTERU3012476,
 30 UTERU3012599, UTERU3012999, UTERU3013167, UTERU3013302,
 UTERU3014274, UTERU3014647, UTERU3014906, UTERU3015011,
 UTERU3015299, UTERU3015647, UTERU3015844, UTERU3016070,
 UTERU3016273, UTERU3016274, UTERU3016308, UTERU3017441,
 UTERU3017626, UTERU3017995, UTERU3018172, UTERU3018255
 35 UTERU2017492, UTERU2025415, UTERU2036507

The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) (Table 20) showed that the genes whose expression levels differed between the two were the 67 and two clones listed below.

5 BRACE2012528, BRAMY4001863, BRAWH3021574, BRAWH3022651,
 BRAWH3024186, BRHIP2027077, BRHIP3001573, BRHIP3002000,
 BRHIP3007223, BRHIP3012997, BRHIP3020046, BRSSN2013696,
 BRSTN2011961, BRSTN2012069, BRTHA2027229, BRTHA2033155,
 BRTHA3011194, BRTHA3022641, CTONG2001932, CTONG2003517,
 10 CTONG2006235, CTONG2008989, CTONG2009033, CTONG2009570,
 CTONG2010330, CTONG2011801, CTONG2012123, CTONG2014206,
 CTONG2014959, CTONG2020582, CTONG2026987, CTONG2027150,
 CTONG2027591, CTONG2027783, CTONG2027959, CTONG3001605,
 CTONG3002518, CTONG3002588, CTONG3003669, CTONG3008223,
 15 NT2RI2009233, NTONG2002278, NTONG2003805, NTONG2004829,
 NTONG2008483, NTONG2009468, OCBBF3004487, PLACE6008315,
 PLACE7004103, SKNMC2003639, SPLEN2012571, SPLEN2019092,
 SYNOV4009575, T1ESE2000904, TESTI2005564, TESTI2018867,
 TESTI4002799, TESTI4005653, TESTI4032913, THYMU3021586,
 20 THYMU3047115, TRACH3006717, TRACH3007625, TRACH3016805,
 TRACH3036932, TRACH3038399, UTERU2000300
 CTONG2002832, CTONG2003764

These genes are involved in cancer.

Expression frequency analysis is used when searching for
 25 genes involved in development and differentiation, where the
 expression levels of genes in developing and/or differentiating
 tissues and/or cells are compared with those in adult tissues
 and/or cells. Genes involved in tissue development and/or
 differentiation are genes which participate in tissue
 30 construction and function expression. These genes are thus
 useful genes available for medicine aiming at regeneration of
 injured tissues.

By using information on gene expression frequency gained
 from the database of the nucleotide sequences of the 1,402,069
 35 clones as described above, genes whose expression frequencies

differed between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, were analyzed.

The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain
 5 (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) (Table 21) showed that the genes whose expression levels differed between the two were the 916 and 13 clones listed below.

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE1000475,
 10 BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336,
 BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838,
 BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126,
 BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397,
 BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992,
 15 BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452,
 BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956,
 BRACE2030039, BRACE2032584, BRACE2033128, BRACE2034434,
 BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607,
 BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975,
 20 BRACE3001403, BRACE3001973, BRACE3002344, BRACE3002541,
 BRACE3002756, BRACE3003866, BRACE3004046, BRACE3004371,
 BRACE3004767, BRACE3004887, BRACE3004981, BRACE3005870,
 BRACE3005903, BRACE3006553, BRACE3007649, BRACE3007869,
 BRACE3009075, BRACE3009265, BRACE3009392, BRACE3009416,
 25 BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774,
 BRACE3013418, BRACE3013874, BRACE3013986, BRACE3014523,
 BRACE3014714, BRACE3015090, BRACE3015898, BRACE3016020,
 BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810,
 BRACE3016862, BRACE3017253, BRACE3018083, BRACE3019570,
 30 BRACE3019611, BRACE3019817, BRACE3019941, BRACE3020356,
 BRACE3020669, BRACE3021430, BRACE3021517, BRACE3021805,
 BRACE3022051, BRACE3022303, BRACE3022312, BRACE3022340,
 BRACE3022847, BRACE3023604, BRACE3024379, BRACE3024444,
 BRACE3024497, BRACE3024537, BRACE3024879, BRACE3025627,
 35 BRACE3025719, BRACE3026161, BRACE3026290, BRACE3026345,
 BRACE3026456, BRACE3026802, BRACE3026844, BRACE3026947,

BRACE3027256, BRACE3027931, BRACE3028360, BRACE3028895,
BRACE3028998, BRACE3029005, BRACE3029021, BRACE3029205,
BRACE3029447, BRACE3030538, BRACE3031161, BRACE3031184,
BRACE3031185, BRACE3031315, BRACE3031372, BRACE3031579,
5 BRACE3031728, BRACE3031743, BRACE3031843, BRACE3032385,
BRACE3032537, BRACE3032538, BRACE3032631, BRACE3032980,
BRACE3033525, BRACE3034183, BRACE3034389, BRACE3034964,
BRACE3034993, BRACE3035168, BRACE3036156, BRACE3036271,
BRACE3036283, BRACE3037612, BRACE3037637, BRACE3037803,
10 BRACE3038012, BRACE3038030, BRACE3038570, BRACE3038760,
BRACE3039288, BRACE3039358, BRACE3039378, BRACE3039454,
BRACE3040012, BRACE3040239, BRACE3040504, BRACE3040644,
BRACE3040863, BRACE3041059, BRACE3041162, BRACE3041827,
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15 BRACE3042432, BRACE3042594, BRACE3043597, BRACE3044090,
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25 BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609,
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30 BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449,
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BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603,
BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234,
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35 BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078,
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BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,
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10 BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
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15 BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
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20 BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
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BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
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25 BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
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30 BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
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35 BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
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5 BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2007525,
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BRCAN2020234, BRCAN2020331, BRCAN2020412, BRCAN2020467,
10 BRCAN2020880, BRCAN2021325, BRCAN2021452, BRCAN2021718,
BRCAN2022126, BRCAN2025093, BRCAN2027593, BRCAN2028702,
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BRCOC2006942, BRCOC2009638, BRCOC2010115, BRCOC2012386,
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15 BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125,
BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735,
BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563,
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20 BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878,
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BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340,
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25 BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710,
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BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294,
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BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753,
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BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185,
35 BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997,
BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675,

BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109,
BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855,
BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880,
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5 BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656,
BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795,
BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160,
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10 BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198,
BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2000312,
BRSTN2006466, BRSTN2006638, BRSTN2008475, BRSTN2009247,
BRSTN2010089, BRSTN2010416, BRSTN2011688, BRSTN2011961,
BRSTN2012069, BRSTN2016892, BRSTN2016918, BRSTN2016992,
15 BRSTN2017104, BRSTN2017151, BRSTN2018712, BRTHA2000969,
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BRTHA2010672, BRTHA2012189, BRTHA2014647, BRTHA2018304,
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20 BRTHA2020642, BRTHA2020695, BRTHA2020721, BRTHA2020781,
BRTHA2020910, BRTHA2021212, BRTHA2021440, BRTHA2021450,
BRTHA2022074, BRTHA2022914, BRTHA2022968, BRTHA2023402,
BRTHA2023437, BRTHA2024177, BRTHA2024354, BRTHA2024712,
BRTHA2025869, BRTHA2026071, BRTHA2026290, BRTHA2026311,
25 BRTHA2027227, BRTHA2027229, BRTHA2027250, BRTHA2028297,
BRTHA2029969, BRTHA2030036, BRTHA2030213, BRTHA2031517,
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30 BRTHA2037247, BRTHA2038279, BRTHA2038345, BRTHA2038353,
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35 BRTHA3011187, BRTHA3011194, BRTHA3011229, BRTHA3011265,
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 BRTHA3017791, BRTHA3018409, BRTHA3018623, BRTHA3019183,
 5 BRTHA3020369, BRTHA3020771, BRTHA3021569, BRTHA3021708,
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 10 BRTHA3027879, BRTHA3027957, BRTHA3028339, BRTHA3028505,
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 CTONG2011801, CTONG2020582, CTONG2027959, D9OST2003106,
 DFNES2001829, FCBBF3001018, FCBBF3002188, FCBBF3005160,
 FCBBF3012443, FCBBF3020030, FCBBF3021191, FCBBF3024911,
 15 FCBBF5000384, FEBRA2000805, FEBRA2002260, FEBRA2012625,
 FEBRA2013069, FEBRA2013570, FEBRA2017736, FEBRA2017811,
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 FEBRA2028457, JCMLC2000273, KIDNE2010049, KIDNE2017153,
 LIVER2008465, MESAN2017133, NOVAR2000783, NT2NE2011107,
 20 NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
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 NT2RP8007920, NT2RP8009119, NTONG2008483, NTONG2009468,
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 OCBBF2009536, OCBBF2014745, OCBBF2016928, OCBBF2018229,
 25 OCBBF2018618, OCBBF2019761, OCBBF2024589, OCBBF2024779,
 OCBBF2025631, OCBBF2030927, OCBBF2036019, OCBBF3000743,
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 SYNOV4009575, T1ESE2000609, T1ESE2000904, TBAES2007428,
 35 TESTI2005112, TESTI2005564, TESTI2009497, TESTI2018867,
 TESTI2021654, TESTI2039342, TESTI4001569, TESTI4002072,

TESTI4002195, TESTI4002774, TESTI4002799, TESTI4003602,
 TESTI4003703, TESTI4003944, TESTI4004210, TESTI4004695,
 TESTI4005013, TESTI4005399, TESTI4005653, TESTI4006441,
 TESTI4007965, TESTI4010979, TESTI4012960, TESTI4013474,
 5 TESTI4014908, TESTI4020596, TESTI4022158, TESTI4029297,
 TESTI4032913, TESTI4035770, TESTI4043223, TESTI4046073,
 THYMU3000776, THYMU3002887, THYMU3003007, THYMU3003350,
 THYMU3007308, THYMU3008105, THYMU3019476, THYMU3021586,
 THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798,
 10 THYMU3032867, THYMU3033626, THYMU3034671, THYMU3037827,
 THYMU3038214, THYMU3041428, THYMU3044075, TKIDN2000319,
 TLIVE2007736, TRACH2013585, TRACH3002752, TRACH3003037,
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 TRACH3007689, TRACH3007995, TRACH3008508, TRACH3008632,
 15 TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885,
 TRACH3021544, TRACH3022109, TRACH3022198, TRACH3024342,
 TRACH3024671, TRACH3025316, TRACH3026303, TRACH3026676,
 TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399,
 TSTOM2000235, UTERU2000300, UTERU2027369, UTERU3000670,
 20 UTERU3005422, UTERU3010409, UTERU3012414, UTERU3013167,
 UTERU3015011, UTERU3016273, UTERU3017995, UTERU3018172
 BRACE3002184, BRACE3026993, BRACE3046450, BRAMY3008096,
 BRAWH3013197, BRAWH3028645, BRTHA3004432, BRTHA3024233,
 CTONG2002832, TESTI4002988, THYMU3046350, TRACH1000193,
 25 TRACH3019290

The result of comparative analysis of cDNA libraries
 derived from fetal heart (FEHRT) and adult heart (HEART) (Table
 22) showed that the genes whose expression levels differed
 between the two were the ten clones listed below.

30 BRACE2012528, BRACE3004371, BRCAN2003814, BRSTN2011961,
 BRSTN2012069, BRSTN2016992, HEART2002531, NTONG2008483,
 PROST2002078, T1ESE2000609

The result of comparative analysis of cDNA libraries
 derived from fetal kidney (FEKID) and adult kidney (KIDNE)
 35 (Table 23) showed that the genes whose expression levels
 differed between the two were the 21 clones listed below.

BRACE3004371, BRAMY2039630, BRAMY3004364, BRAWH2004078,
 BRHIP3002000, BRSTN2011961, BRSTN2012069, BRTHA2027229,
 KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987,
 KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RP7007387,
 5 TESTI2005112, TESTI4002799, THYMU3001776, THYMU3029795,
 THYMU3032867

The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) (Table 24) showed that the genes whose expression levels differed
 10 between the two were the 18 clones listed below.

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069,
 HLUNG2012600, MESAN2009156, NTONG2008483, PROST2007444,
 TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297,
 THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428,
 15 THYMU3044188, TRACH3022198

These genes are involved in regeneration of tissues and/or cells.

For example, if a polypeptide encoded by a cDNA of the present invention is a regulatory factor for cellular conditions
 20 such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the present invention is injected into cells using microinjection, and then low molecular weight compounds and such can be screened by using, as an index, change in cellular
 25 conditions (such as growth and differentiation), or activation/inhibition of a particular gene in the cell. The screening can be performed as follows.

A polypeptide of the present invention is first expressed and purified as a recombinant. This purified polypeptide is
 30 then microinjected into cells such as various cell lines, or primary culture cells, and cellular changes such as growth and differentiation are examined. Alternatively, induction of a gene whose expression is known to be involved in the change of a particular cellular condition may be detected using mRNA or
 35 polypeptide amounts. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.)

may be detected, where that amount is changed by the function of a gene product (polypeptide) known to influence change in a particular cellular condition. The compounds to be screened (including both low and high molecular compounds) can be added to culture media and screened using, as an index, their ability to change a cellular condition.

Cell lines introduced with a gene of the present invention can be used for screening, even without microinjection. If the product of a gene of the present invention is revealed to be involved in a particular change in cellular conditions, the change in that product can be used as an index for screening. Once a compound which can activate or inhibit the function of a polypeptide of the present invention has been developed using this screening, such a compound can be practically applied in medicines.

If a polypeptide encoded by a cDNA of the present invention is a secretory or membrane protein, or a protein involved in signal transduction, glycoproteins, transcription, or disease, it can be used in functional assays for developing medicines as described below.

In case of a membrane protein, the polypeptide is very likely to function as a receptor or ligand on the cell surface. Therefore, it is possible to reveal new ligand-receptor relationships by screening membrane proteins of the present invention, based on binding activity with known or new ligands or receptors. Screening can be performed according to known methods.

For example, a ligand against a polypeptide of the present invention can be screened in the following manner. Namely, a ligand that binds to a specific polypeptide can be screened using a method comprising the steps of: (a) contacting a test sample with a polypeptide of the present invention, or partial peptide thereof, or cells expressing such, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

Screening using cells expressing receptor polypeptides of the present invention can also be performed, for example, as follows. Receptors capable of binding to a specific polypeptide can be screened by (a) attaching sample cells to a polypeptide
5 of the present invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

For example, screening can be carried out as follows: a polypeptide of the present invention is first expressed, the
10 recombinant polypeptide is purified and labeled, a binding assay is performed using various cell lines or primary cultured cells, and cells that express the receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu
15 edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the present invention can be labeled with RI such as ^{125}I , and enzyme (alkaline phosphatase etc.).

Alternatively, a polypeptide of the present invention may be used without labeling and then detected by using a labeled
20 antibody against that polypeptide. Cells expressing a receptor polypeptide of the present invention, and selected using the above screening methods, can be applied as mentioned below to screen agonists or antagonists of that receptor.

Once a ligand binding to a polypeptide of the present
25 invention, a receptor of that polypeptide, or cells expressing that receptor have been obtained by screening as described above, a compound binding to that ligand or receptor can be screened. It is also possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example)
30 by using this binding activity as an index.

When a polypeptide of the present invention is a receptor, the screening method comprises the steps of (a) contacting the
ligand with a polypeptide of the present invention, or cells expressing that polypeptide, in the presence of a test sample,
35 (b) detecting binding activity between that polypeptide or cells expressing that polypeptide and the ligand, and (c) selecting a

compound that can reduce that binding activity when compared to activity in the absence of the test sample. Furthermore, when a polypeptide of the present invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of
5 the present invention with its receptor or cells expressing that receptor, in the presence of a test sample, (b) detecting binding activity between the polypeptide and its receptor, or cells expressing that receptor, and (c) selecting a compound that can reduce that binding activity compared to activity in
10 the absence of the test sample.

Examples of test samples to screen include, but are not limited to, cell extracts, expressed gene library products, synthesized low molecular compounds, synthesized peptides, and natural compounds. A compound that is isolated by the above
15 screening can also be used as a test sample, using binding activity with a polypeptide of the present invention as an index.

A compound isolated using this screening may be a candidate agonist or antagonist of a polypeptide or polypeptide receptor of the present invention. By monitoring changes in
20 intracellular signals, such as phosphorylation due to reduced binding between a polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the polypeptide receptor of the present invention. Also, the screened compound may be a candidate for a compound
25 that can inhibit interaction between a polypeptide and its associated molecules (including receptors) *in vivo*. The polypeptides of this invention, receptors that bind to those polypeptides or ligands, and compounds thereof, can be applied in the development of preventative, therapeutic or testing
30 agents for diseases in which the polypeptides of the present invention are involved.

Secretory proteins may regulate cellular conditions such as growth and differentiation. A novel factor that regulates cellular conditions can be found by i) adding a secretory
35 protein of the present invention to a certain kind of cell, and

ii) screening using as an index cellular changes in growth or differentiation, or activation of a particular gene.

Screening can be performed, for example, as follows. First, a polypeptide of the present invention is expressed and purified
5 in a recombinant form. Then, the purified polypeptide is added to various cell lines or primary cultured cells, and changes in cell growth and differentiation are monitored. The induction of a particular gene known to be involved in a certain cellular change is detected using mRNA and polypeptide amounts.
10 Alternatively, detection can be carried out using the amount of an intracellular molecule (low-molecular-weight compounds, etc.) changed by the action of a gene product (polypeptide) which influences a certain cellular change.

If screening reveals that a polypeptide of the present
15 invention can regulate cellular conditions or functions, it is possible to apply that polypeptide as a pharmaceutical and diagnostic medicine for related diseases, either directly or by altering a part of it into an appropriate composition.

As for membrane proteins as described above, a secretory
20 protein provided by the present invention may be used to explore a novel ligand-receptor interaction by screening based on binding activity to a known or new ligand or receptor. A similar method can be used to identify an agonist or antagonist. Compounds obtained by these methods are candidate compounds for
25 inhibiting the interaction between the polypeptide of the present invention and an interacting molecule (including receptors). These compounds may be applied as preventive, therapeutic, or testing agents for diseases in which the polypeptide plays a role.

30 Proteins involved in signal transduction or transcription may be factors that affect a certain polypeptide or gene in response to intra- or extra-cellular stimuli. A novel factor able to affect a polypeptide or gene can be found by expressing a polypeptide provided by the present invention in a certain
35 type of cell, and screening using as an index the activation of a certain intracellular polypeptide or gene.

Screening may be performed as follows. First, a transformed cell line which expresses a polypeptide of the present invention is obtained. Then, changes in a certain gene between the transformed and the original untransformed cell lines are detected using mRNA or polypeptide amounts. Alternatively, detection may be carried out using the amount of an intracellular molecule (low molecular weight compounds, etc.) changed by the function of a certain gene product (polypeptide). Furthermore, change in expression of a certain gene can be detected by estimating the activity of a marker gene product (polypeptide), where the polypeptide of the present invention is expressed in a cell that has been introduced with a fusion gene comprising a regulatory region of the certain gene and a marker gene (luciferase, β -galactosidase, etc.).

If the polypeptide or gene influenced by a protein of the present invention is involved in disease, it is possible to screen a gene or compound that can regulate that polypeptide or gene's expression and/or activity, either directly or indirectly, by utilizing a polypeptide of the present invention.

For example, a polypeptide of the present invention is expressed and purified as a recombinant polypeptide, and a polypeptide or gene that interacts with that polypeptide is purified and screened based on binding. Alternatively, changes in binding activity can be monitored after adding a candidate inhibitor compound. In another method, the 5'-upstream transcription regulatory region of a gene that encodes a polypeptide of the present invention and that can regulate the expression of another gene, is obtained. The gene is fused with a marker gene and then introduced into a cell, compounds and the like are added, and a factor which can regulate expression of that gene can be discovered.

A compound obtained by this screening can be used for developing pharmaceutical medicines for a disease in which a polypeptide of the present invention is involved. Similarly, if a regulatory factor obtained by screening turns out to be a polypeptide, compounds that can newly affect the expression or

activity of this polypeptide may be used as a medicine for diseases in which the polypeptide of the present invention is involved.

5 If a polypeptide of the present invention has enzymatic activity, regardless of whether it is a secretory protein, membrane protein, or a protein involved in signal transduction, glycoprotein, transcription, or disease, screening may be performed by adding a compound to the polypeptide of the present invention under suitable conditions, and monitoring that
10 compound's change. This enzymatic activity may also be used as an index to screen a compound that inhibits the polypeptide activity.

In an example of this screening, a polypeptide of the present invention is expressed and the recombinant polypeptide
15 is purified. Then, compounds are contacted with the purified polypeptide, and the amount of compound and reaction product is examined. Alternatively, inhibitor candidate compounds are added, then a compound (substrate) that reacts with the purified polypeptide is added, and change in the amount of substrate and
20 reaction product is examined.

A compound obtained by screening may be used as a medicine for diseases in which a polypeptide of the present invention is involved. Also such a compound can be applied in tests that examine, for example, whether a polypeptide of the invention
25 functions normally *in vivo*.

Whether a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in disease or not is determined using
30 different method to that described above. In this method, a specific antibody against a polypeptide of the present invention is obtained, and the relationship between the expression or activity of the polypeptide and a certain disease is examined. Alternatively, analysis can use the methods in "Molecular
35 Diagnosis of Genetic Diseases" as a reference (Elles R. edit,

(1996) in the series of "Method in Molecular Biology" (Humana Press).

Proteins involved in disease are very useful in developing drugs which regulate their expression and activity, and become
5 targets of the above-mentioned screenings. They are also useful in the medicinal industry as diagnostic markers for their related disease, or as gene therapy targets.

A compound isolated as mentioned above can be administered to patients as is, or after being formulated into a
10 pharmaceutical composition according to known methods. Specific examples of pharmaceutically acceptable carriers or vehicles include sterilized water, saline, plant oils, emulsifiers, suspending agents and the like, where they are mixed with the compound appropriately. The pharmaceutical compositions can be
15 administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injection. Dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can properly choose an appropriate dosage. If a
20 compound is encoded by a polynucleotide, the polynucleotide can be cloned into a gene therapy vector, and used for gene therapy. Those skilled in the art can properly choose the dosage of the polynucleotide and the method of its administration, and these may vary depending on the weight, age or symptoms of a patient.

25 The present invention further relates to databases comprising at least one sequence of a polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotides and/or amino acids indicated in Table 1. The term "database" means a set of
30 accumulated, machine-searchable and readable nucleotide sequence information. The databases of the present invention comprise at least one of the novel nucleotide sequences of the polynucleotides provided by the present invention. The databases of the present invention can consist only of the
35 sequence data of the novel polynucleotides provided by the present invention, or can comprise other information on known

nucleotide sequences of full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only information on nucleotide sequences, but also information on gene functions as revealed by the present invention. Additional
5 information such as the names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

The database of the present invention is useful for gaining complete gene sequence information from the partial sequence
10 information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method,
15 information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

Sequence information of the full-length cDNAs constituting the database of the present invention contains information on
20 not only complete sequences, but also on gene expression frequency and gene homology to known genes and polypeptides. This extra information facilitates rapid functional analyses of partial gene fragments. Further, information on human genes is accumulated in the database of the present invention, and
25 therefore, the database is useful for isolating a human homologue of a gene originating from another species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

At present, information on a wide variety of gene fragments
30 can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to a known gene, the full-length sequence is easily obtained by comparing the partial sequence with the
35 information in known databases. However, when there is no information corresponding to the partial sequence of interest in

known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using partial sequence information as an initial clue. If the full-length gene is not available, the amino acid sequence of the polypeptide encoded by that gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed using databases of known genes.

The present invention has provided 1,995 polynucleotides. In humans, where isolation of full-length cDNA has not progressed, the provision of new full-length cDNAs has great significance. Secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are known to be involved in many diseases. The genes and proteins involved in diseases are useful for developing diagnostic markers or medicines for regulation of their expression and activity, or as a gene therapy target.

In particular, cDNA encoding secretory proteins of the present invention are extremely important to the industry since these proteins are expected to be useful as pharmaceutical agents, and many disease-related genes can be included with them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding these proteins can be used as disease indexes, etc. These cDNAs are also very important to the industry, and are expected to be effective in treating diseases and the like by regulating the activity or expression of the proteins they encode.

[Industrial Applicability]

Human cDNAs involved in various diseases, morbid states, or functions were isolated in the present invention. The cDNAs of the present invention include, for example, genes that can be useful as diagnostic markers or therapeutic targets for the diseases or morbid states shown below. These diseases receive

widespread attention, and require the development of new technology for treatment and diagnosis.

- osteoporosis
- neurologic diseases
- 5 • Alzheimer's disease
- Parkinson's disease
- dementia
- various cancers

10 In addition, human cDNAs involved in the functions shown below were isolated in the present invention. These genes can be used to elucidate the mechanisms of various functions, and in therapeutic methods which enhance or repress those functions. For example, genes participating in tissue generation and functional expression can be used in regenerative medicines.

- 15 • emotional reaction
- tissue generation and functional expression
- motor function controlled by the brain, signaling function controlled by the brain
- emotional reaction, fear response, and panic

20 Furthermore, information on the nucleotide sequence of the full-length cDNAs or their full-length amino acid sequences as provided by the present invention can be used to isolate human genes based on partial sequence information obtained by functional analysis of various genes, or from sequence
25 information of genes from non-human organisms.

Any patents, patent applications, and publications cited herein are incorporated by reference.

The present invention is illustrated more specifically with reference to the following examples, but is not to be
30 construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA

35 Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method described in the reference

(J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989). Further, by the method described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) cultivated by the methods described in the catalogs.

The library names and origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Extraction of mRNA from human tissues>

NTONG: Normal tongue;

CTONG: Tongue cancer;

FCBBF: Fetal brain;

OCBBF: Fetal brain;

PLACE: Placenta;

SYNOV: Synovial membrane tissue (from rheumatioid arthritis);

CORDB: Cord blood.

<Extraction of mRNA from culture cells>

BNGH4: H4 cells (ATCC #HTB-148);

IMR32: IMR32 cells (ATCC #CCL-127);

SKNMC: SK-N-MC cells (ATCC #HTB-10);

3NB69: NB69 cells (RCB #RCB0480);

BGGI1: GI1 cells (RCB #RCB0763);

NB9N4: NB9 cells (RCB #RCB0477);

SKNSH: SK-N-SH cells (RCB #RCB0426);

AHMSC: Human mesenchymal cells (HMSC);

CHONS: Chondrocytes;

ERLTF: TF-1 cells (Erythroleukemia);

HELAC: HeLa cells;

JCMCLC: Myelogenous leukemia cells;

MESTC: Mesenchyme stem cells;

N1ESE: Mesenchymal stem cells;

NCRRM: Embryonal carcinomas;

NCRRP: Embryonal carcinomas treated with retinoic acid (RA) to induce the differentiation;

TlESE: Mesenchymal stem cells treated with trichostatin and 5-azacytidine to induce the differentiation;

5 NT2RM: NT2 cells (STARATAGENE #204101);

NT2RP: NT2 cells treated with RA for 5 weeks to induce the differentiation;

10 NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks;

NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron);

15 NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for five weeks to induce the differentiation, and then treated with the growth inhibitor for two weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNA libraries whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a
20 Subtract Kit (Invitrogen #K4320-01); the subtracted library (NT2RI-NT2RM) was provided by this procedure.

RCB indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American
25 Type Culture Collection.

<Extraction of mRNA from primary culture cells>

ASTRO: Normal human astrocyte NHA5732, Takara Shuzo #CC2565;

DFNES: Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;

30 MESAN: Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;

NHNPC: Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;

35 PEBLM: Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;

HSYRA: Human synoviocyte HS-RA (from rheumatoid arthritis),
Toyobo #T404K-05;

PUAEN: Normal human pulmonary artery endothelial cells, Toyobo
#T302K-05;

5 UMVEN: Normal human umbilical vein endothelial cell HUVEC,
Toyobo #T200K-05;

HCASM: Normal human coronary artery smooth muscle cell HCASM, Toyobo
#T305K-05;

HCHON: Normal human chondrocyte HC, Toyobo #T402K-05;

10 HHDPC: Normal human dermal papilla cell HDPC, Toyobo #THPCK-001;

CD34C: CD34+ cells (AllCells, LLC #CB14435M);

D3OST: CD34+ cells treated with the osteoclast differentiation
factor (ODF) for three days to induce the differentiation;

15 D6OST: CD34+ cells treated with ODF for six days to induce the
differentiation;

D9OST: CD34+ cells treated with ODF for nine days to induce the
differentiation;

ACTVT: Activated T-cells;

LYMPB: Lymphoblasts (EB virus transferred B cells);

20 NETRP: Neutrophils.

Total RNAs extracted from the following human tissues were
then purchased and used as mRNA sources. Library names and the
origins are indicated below in the order of "Library name:
Origin". When a library was prepared by the subtraction method,
25 the item is followed by a description of how to prepare the
subtracted library.

<Purchase of total RNA containing mRNA extracted from human
tissues>

ADRGL: Adrenal gland, CLONTECH #64016-1;

30 BRACE: Brain (cerebellum), CLONTECH #64035-1;

BRAWH: Whole brain, CLONTECH #64020-1;

FEBRA: Fetal brain, CLONTECH #64019-1;

FELIV: Fetal liver, CLONTECH #64018-1;

HEART: Heart, CLONTECH #64025-1;

35 HLUNG: Lung, CLONTECH #64023-1;

KIDNE: Kidney, CLONTECH #64030-1;

LIVER: Liver, CLONTECH #64022-1;
MAMGL: Mammary Gland, CLONTECH #64037-1;
PANCR: Pancreas, CLONTECH #64031-1;
PROST: Prostate, CLONTECH #64038-1;
5 SALGL: Salivary Gland, CLONTECH #64026-1;
SKMUS: Skeletal Muscle, CLONTECH #64033-1;
SMINT: Small Intestine, CLONTECH #64039-1;
SPLEN: Spleen, CLONTECH #64034-1;
STOMA: Stomach, CLONTECH #64090-1;
10 TBAES: Breast (Tumor), CLONTECH #64015-1;
TCERX: Cervix (Tumor), CLONTECH #64010-1;
TCOLN: Colon (Tumor), CLONTECH #64014-1;
TESTI: Testis, CLONTECH #64027-1;
THYMU: Thymus, CLONTECH #64028-1;
15 TLUNG: Lung (Tumor), CLONTECH #64013-1;
TOVAR: Ovary (Tumor), CLONTECH #64011-1;
TRACH: Trachea, CLONTECH #64091-1;
TUTER: Uterus (Tumor), CLONTECH #64008-1;
UTERU: Uterus, CLONTECH #64029-1;
20 ADIPS: Adipose, Invitrogen #D6005-01;
BLADE: Bladder, Invitrogen #D6020-01;
BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex,
Alzheimer), Invitrogen #D6830-01;
CERVX: Cervix, Invitrogen #D6047-01;
25 COLON: Colon, Invitrogen #D6050-0;
NESOP: Esophagus, Invitrogen #D6060-01;
PERIC: Pericardium, Invitrogen #D6105-01;
RECTM: Rectum, Invitrogen #D6110-01;
TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
30 TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
TLIVE: Liver (Tumor), Invitrogen #D6880-01;
TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
BEAST: Adult breast, STARATAGENE #735044;
FEHRT: Fetal heart, STARATAGENE #738012;
35 FEKID: Fetal kidney, STARATAGENE #738014;
FELNG: Fetal lung, STARATAGENE #738020;

NOVAR: Adult ovary, STARATAGENE #735260;

BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was constructed from mRNA prepared from tissues of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01]; the cDNA libraries whose nucleotide sequences were shared by those of mRNAs from whole brain tissue [BRAWH: Whole brain, CLONTECH #64020-1] were subtracted using a Subtract Kit (Invitrogen #K4320-01).

Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were purchased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue was combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and origins are indicated below in the order of "Library name: Origin".

<Purchase of mRNAs of human tissues as poly A(+) RNAs>

BRAMY: Brain (amygdala), CLONTECH #6574-1;

BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;

BRCOC: Brain (corpus callosum), CLONTECH #6577-1;

BRHIP: Brain (hippocampus), CLONTECH #6578-1;

BRSSN: Brain (substantia nigra), CLONTECH #6580-1;

BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;

BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA libraries

A cDNA library was prepared from each RNA using the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (agcaucgagu cggccuuguu ggccuacugg/ SEQ ID NO: 3991) and oligo dT primer (gcggctgaag acggcctatg tggccttttt tttttttttt tt/ SEQ ID NO: 3992), as described in WO 01/04286. The single-

stranded cDNA was then converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (agcatcgagt cggccttggtg/ SEQ ID NO: 3993) and 3' (gcggctgaag acggcctatg t/ SEQ ID NO: 3994) PCR primers, and then digested with *Sfi*I. Then, a
 5 fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dra*III-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); and the cDNA library was thus prepared.

Shown below are the names of cDNA libraries used in the
 10 analysis of full-length cDNA sequences, and their origins. The Library Name is provided with the Type, Origin, and such of the library source, demarcated by a slash mark (/) within parentheses.

3NB69 (culture cells / NB69 cells (RCB #RCB0480))
 15 ADIPS (Tissues / Adipose (Invitrogen #D6005-01))
 ADRGL (Tissues / Adrenal gland (CLONTECH #64016-1))
 AHMSC (culture cells / HMSC cells (Human mesenchymal cell))
 ASTRO (primary culture cells / Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565))
 20 BEAST (Tissues / Adult Breast (STARATAGENE #735044))
 BLADE (Tissues / Bladder (Invitrogen #D6020-01))
 BRACE (Tissues / Brain (cerebellum) (CLONTECH #64035-1))
 BRALZ (Tissues / Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer) (Invitrogen #D6830-01))
 25 BRAMY (Tissues / Brain (amygdala) (CLONTECH #6574-1))
 BRAWH (Tissues / Whole brain (CLONTECH #64020-1))
 BRCAN (Tissues / Brain (caudate nucleus) (CLONTECH #6575-1))
 BRCOC (Tissues / Brain (corpus callosum) (CLONTECH #6577-1))
 BRHIP (Tissues / Brain (hippocampus) (CLONTECH #6578-1))
 30 BRSSN (Tissues / Brain (substantia nigra) (CLONTECH #6580-1))
 BRSTN (Tissues / Brain (subthalamus nucleus) (CLONTECH #6581-1))
 BRTHA (Tissues / Brain (thalamus) (CLONTECH #6582-1))
 CERVX (Tissues / Cervix (Invitrogen #D6047-01))
 CHONS (culture cells / Chondrocyte)
 35 COLON (Tissues / Colon (Invitrogen #D6050-0))
 CTONG (Tissues / Tongue Cancer)

- D9OST (primary culture cells / CD34+ cells (treated with ODF for nine days to induce the differentiation))
- DFNES (primary culture cells / Normal human dermal fibroblasts (neonatal skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509))
- 5 ERLTF (culture cells / TF-1 cells (Erythroleukemia))
- FCBBF (Tissues / Fetal brain)
- FEBRA (Tissues / Fetal brain (CLONTECH #64019-1))
- FEHRT (Tissues / Fetal heart (STARATAGENE #738012))
- FEKID (Tissues / Fetal kidney)
- 10 FELNG (Tissues / Fetal lung (STARATAGENE #738020))
- HCASM (primary culture cells / Normal human coronary artery smooth muscle cell HCASMC (Toyobo #T305K-05))
- HCHON (primary culture cells / Normal human chondrocyte HC (Toyobo #T402K-05))
- 15 HEART (Tissues / Heart (CLONTECH #64025-1))
- HHDPC (primary culture cells / Normal human dermal papilla cell HDPC (Toyobo #THPCK-001))
- HLUNG (Tissues / Lung (CLONTECH #64023-1))
- HSYRA (primary culture cells / Human synoviocyte HS-RA (from
- 20 rheumatoid arthritis) (Toyobo #T404K-05))
- JCMLC (culture cells / myelogenous leukemias)
- KIDNE (Tissues / Kidney (CLONTECH #64030-1))
- LIVER (Tissues / Liver (CLONTECH #64022-1))
- LYMPB (primary culture cells / Lymphoblasts (EB virus
- 25 transferred B cells))
- MESAN (primary culture cells / Normal human mesangial cell NHMC56046-2 (Takara Shuzo #CC2559))
- MESTC (culture cells / Mesenchyme stem cells)
- N1ESE (culture cells / Mesenchyme stem cells)
- 30 NETRP (primary culture cells / Neutrophil)
- NOVAR (Tissues / Adult ovary (STARATAGENE #735260))
- NT2NE (culture cells / NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron))

NT2RI (culture cells / NT2 cells treated with RA for five weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks)

NT2RP (culture cells / NT2 cells treated with RA for five weeks

5 to induce the differentiation)

NTONG (Tissues / Normal tongue)

OCBBF (Tissues / Fetal brain)

PEBLM (primary culture cells / Normal human peripheral blood mononuclear cell HPBMC5939 (Takara Shuzo #CC2702))

10 PERIC (Tissues / Pericardium (Invitrogen #D6105-01))

PLACE (Tissues / Placenta)

PROST (Tissues / Prostate (CLONTECH #64038-1))

PUAEN (primary culture cells / Normal human pulmonary artery endothelial cells (Toyobo #T302K-05))

15 RECTM (Tissues / Rectum (Invitrogen #D6110-01))

SKMUS (Tissues / Skeletal Muscle (CLONTECH #64033-1))

SKNMC (culture cells / SK-N-MC cells (ATCC #HTB-10))

SKNSH (culture cells / SK-N-SH cells (RCB #RCB0426))

SMINT (Tissues / Small Intestine (CLONTECH #64039-1))

20 SPLEN (Tissues / Spleen (CLONTECH #64034-1))

STOMA (Tissues / Stomach (CLONTECH #64090-1))

SYNOV (Tissues / Synovial membrane tissue (from rheumatoid arthritis))

T1ESE (culture cells / Mesenchymal stem cell (treated with

25 trichostatin and 5-azacytidine to induce the differentiation))

TBAES (Tissues / Breast (Tumor) (CLONTECH #64015-1))

TESOP (Tissues / Esophageal (Tumor) (Invitrogen #D6860-01))

TESTI (Tissues / Testis (CLONTECH #64027-1))

THYMU (Tissues / Thymus (CLONTECH #64028-1))

30 TKIDN (Tissues / Kidney (Tumor) (Invitrogen #D6870-01))

TLIVE (Tissues / Liver (Tumor) (Invitrogen #D6880-01))

TLUNG (Tissues / Lung (Tumor))

TRACH (Tissues / Trachea (CLONTECH #64091-1))

TSTOM (Tissues / Stomach (Tumor) (Invitrogen #D6920-01))

35 TUTER (Tissues / Uterus (Tumor) (CLONTECH #64008-1))

UTERU (Tissues / Uterus (CLONTECH #64029-1))

cdNA libraries with a high fullness ratio (the fullness ratio of 5'-end was 90% on average, calculated for each cdNA library using the protein coding region found in known mRNA species as an index) prepared by the improved oligo-capping method were constructed using a eukaryotic expression vector pME18SFL3. The vector contained SR α promoter and SV40 small t intron upstream of the cloning site, and SV40 polyA added signal sequence site downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cdNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cdNA fragments can be inserted downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cdNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, clones can be analyzed very easily using the clone gene product proteins, or those proteins' biological activities.

(3) Assessment of 5'-end completeness of clones derived from a cdNA library prepared by oligo-capping

With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cdNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction were conducted using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

The 5'-end completeness of about 1,110,000 clones derived from the human cdNA libraries prepared by the improved oligo-capping method was determined using the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA. Even if the 5'-end sequence was shorter, clones containing the translation initiation codon were judged to comprise the "full-length" sequence. Clones which did not

comprise the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparison with known human mRNA. The fullness ratio of the 5'-ends was found to be 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in human cDNA clones obtained by the oligo-capping method.

EXAMPLE 2

Sequencing analysis of cDNA ends and selection of full-length clones

With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequences, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search;

when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

5

EXAMPLE 3

Analysis of the full-length nucleotide sequences

The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was
10 mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier
15 using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids
20 containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

25 Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOS corresponding to the respective sequences are shown in Table 1.

30

EXAMPLE 4

Functional prediction by homology search

SwissProt, RefSeq, and nr were searched using BLAST for the determined nucleotide sequences and the ORF amino acid sequences deduced to encode the polypeptides. Of the hit data which met
35 the criteria described below, representative hit data were selected. This representative data is hit data with a higher

homology and that enables relatively easy functional prediction for nucleotide sequences and deduced amino acid sequences. The results of the homology search are shown at the end of this specification.

- 5 · Hit data whose P value or E value is 10^{-4} or less
- For analysis using an amino acid database, hit data whose P value or E value is 10^{-4} or less, where the length of consensus sequence \times homology = 30 or higher,

Thus, only representative data are indicated and molecules
 10 exhibiting homology to each clone are not limited thereto. For some clones, hit data that do not meet the above-described criteria in BLAST search are not shown.

EXAMPLE 5

15 Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the
 20 presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)]
 25 (Mitsui Knowledge Industry); the function domain, by Pfam (Version 5.5) (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by
 30 PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE
 35 (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). In addition,

the functional domain search can also be carried out on the PROSITE.

The search results obtained with the respective programs are shown below.

5 The 130 clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADIPS2000069, ASTRO2015162, BEAST2000981, BLADE2001031, BRACE2017397, BRACE2023633, BRACE3009392, BRACE3013986, BRACE3014523, BRACE3026345, BRACE3032537, BRACE3037803, 10 BRACE3051144, BRAMY2015516, BRAMY3002886, BRAMY3009556, BRAMY3016829, BRAWH2011958, BRAWH2016209, BRAWH3005886, BRAWH3012005, BRAWH3014609, BRAWH3016123, BRAWH3018063, BRAWH3020200, BRAWH3023421, BRAWH3028223, BRAWH3032298, BRAWH3034134, BRAWH3040695, BRAWH3042438, BRAWH3046196, 15 BRAWH3049068, BRCAN2003269, BRCAN2006955, BRCAN2018269, BRHIP2006921, BRHIP2020930, BRHIP3000859, BRHIP3012997, BRHIP3016032, BRHIP3020046, BRHIP3020733, BRHIP3028742, BRHIP3030230, BRHIP3035754, BRSSN2018218, BRSTN2010089, BRSTN2011688, BRTHA2000969, BRTHA2014647, BRTHA2020400, 20 BRTHA2020721, BRTHA2026290, BRTHA2030036, BRTHA2033320, BRTHA2033683, BRTHA3003225, BRTHA3014835, BRTHA3018623, BRTHA3026161, BRTHA3027820, COLON2005623, CTONG3002588, FEBRA2023498, FEKID2002493, HCHON2009766, JCMLC2002095, NETRP2004090, NETRP2005849, NT2RI3009524, NT2RP8008057, 25 OCBBF3007704, OCBBF3021502, OCBBF3022123, OCBBF3028001, PEBLM2005615, SKMUS2008585, SPLEN2025012, SPLEN2035615, SPLEN2042051, STOMA2004663, SYNOV4009139, TESTI2037657, TESTI2049041, TESTI4002072, TESTI4022158, TESTI4024494, TESTI4035872, TESTI4043371, TESTI4045168, THYMU3003350, 30 THYMU3014173, THYMU3015457, THYMU3023107, THYMU3025118, THYMU3025313, THYMU3025642, THYMU3026532, THYMU3026869, THYMU3028461, THYMU3029795, THYMU3034099, THYMU3036310, THYMU3036953, THYMU3037772, THYMU3038158, THYMU3038167, THYMU3040068, THYMU3040746, THYMU3044188, THYMU3045510, 35 THYMU3047542, TRACH3003872, TRACH3014580, TRACH3016368, TRACH3019058, TRACH3020930, TRACH3021023, TRACH3021544,

TRACH3022758, TRACH3023203, TRACH3023516, TRACH3025346,
 TRACH3026542, TRACH3026650, TRACH3029670, TRACH3031316,
 TRACH3034680, TRACH3036278

Deduced amino acid sequences of following nine clones were
 5 also detected to have the signal sequences by PSORT.

ADRGL2011190, PROST2010326, TBAES2004105, TBAES2007379,
 TBAES2008133, THYMU3044175, TLIVE2007192, UTERU2025415,
 UTERU2036507

The 455 clones whose deduced amino acid sequences were
 10 detected to have the transmembrane domains by SOSUI are as
 follows. Numerals indicate the numbers of transmembrane domains
 detected in the deduced amino acid sequences. Of the search
 result, the Clone Name and the Number of transmembrane domains
 are demarcated by a double slash mark (//).

15 3NB692004045//5, ADRGL2010315//3, ASTRO2015162//5,
 BEAST2000981//4, BLADE2002744//2, BLADE2007744//1,
 BRACE2003628//4, BRACE2012528//1, BRACE2013126//3,
 BRACE2017580//2, BRACE2017992//2, BRACE2023633//2,
 BRACE2030039//6, BRACE2035191//1, BRACE3001973//2,
 20 BRACE3002264//11, BRACE3002344//1, BRACE3004981//1,
 BRACE3007869//3, BRACE3009392//6,
 BRACE3013874//2, BRACE3015898//1, BRACE3018083//1,
 BRACE3021517//1, BRACE3021805//1, BRACE3022051//1,
 BRACE3024379//2, BRACE3024444//2, BRACE3024497//2,
 25 BRACE3024879//6, BRACE3026345//1, BRACE3026456//1,
 BRACE3026802//2, BRACE3028360//2, BRACE3029021//1,
 BRACE3030538//5, BRACE3031372//3, BRACE3031579//3,
 BRACE3031728//1, BRACE3032385//8,
 BRACE3032980//1, BRACE3033525//1, BRACE3034964//1,
 30 BRACE3034993//2, BRACE3037637//3, BRACE3037803//2,
 BRACE3038570//3, BRACE3039358//1, BRACE3039378//6,
 BRACE3040644//1, BRACE3040863//2, BRACE3042326//11,
 BRACE3042409//4, BRACE3042432//2, BRACE3044090//2,
 BRACE3046049//1, BRACE3046152//3, BRACE3046466//2,
 35 BRACE3048565//2, BRACE3050504//7,
 BRACE3051144//3, BRACE3051621//3, BRACE3052486//1,

BRALZ2011337//1, BRALZ2013690//2, BRAMY2015516//4,
 BRAMY2021098//1, BRAMY2025495//2, BRAMY2037609//2,
 BRAMY2040915//1, BRAMY2041507//2, BRAMY2044686//4,
 BRAMY2046537//5, BRAMY3002886//5, BRAMY3004126//6,
 5 BRAMY3007449//2, BRAMY3009904//2, BRAMY3010654//2,
 BRAMY3010902//2, BRAMY3015547//2,
 BRAMY3015549//2, BRAMY3016829//3, BRAWH2000256//5,
 BRAWH2010364//2, BRAWH2011812//1, BRAWH2012866//1,
 BRAWH2016209//5, BRAWH2016305//1, BRAWH3001053//1,
 10 BRAWH3001783//1, BRAWH3001833//7, BRAWH3005892//1,
 BRAWH3008867//2, BRAWH3010461//4, BRAWH3010657//1,
 BRAWH3011907//1, BRAWH3012662//1, BRAWH3012779//3,
 BRAWH3013049//1, BRAWH3014609//2,
 BRAWH3015175//1, BRAWH3018063//1, BRAWH3018969//5,
 15 BRAWH3019529//1, BRAWH3019820//3, BRAWH3020200//3,
 BRAWH3020884//1, BRAWH3021012//2, BRAWH3021641//2,
 BRAWH3022347//1, BRAWH3023156//1, BRAWH3023274//2,
 BRAWH3023415//1, BRAWH3024186//1, BRAWH3024242//3,
 BRAWH3027574//1, BRAWH3027880//5, BRAWH3028223//2,
 20 BRAWH3028754//2, BRAWH3029806//10,
 BRAWH3030810//1, BRAWH3034114//1, BRAWH3034134//1,
 BRAWH3035914//1, BRAWH3036270//1, BRAWH3038055//1,
 BRAWH3038324//3, BRAWH3040695//1, BRAWH3040711//2,
 BRAWH3042132//1, BRAWH3042438//1, BRAWH3042772//2,
 25 BRAWH3042996//2, BRAWH3043498//2, BRAWH3044676//1,
 BRAWH3046196//3, BRAWH3047063//1, BRAWH3048374//2,
 BRAWH3048724//2, BRAWH3049068//2,
 BRAWH3049544//1, BRCAN2002662//1, BRCAN2003269//3,
 BRCAN2018269//2, BRCAN2019653//2, BRCAN2020412//2,
 30 BRCAN2020972//1, BRCAN2022126//5, BRCOC2006164//8,
 BRCOC2006639//1, BRCOC2009638//3, BRHIP2021929//7,
 BRHIP3001878//3, BRHIP3002000//10, BRHIP3002124//3,
 BRHIP3003306//2, BRHIP3003395//1, BRHIP3004774//1,
 BRHIP3005801//1, BRHIP3006950//2,
 35 BRHIP3007195//8, BRHIP3007960//1, BRHIP3008320//6,
 BRHIP3010289//2, BRHIP3011831//1, BRHIP3012185//2,

BRHIP3013078//1, BRHIP3016032//10, BRHIP3017146//3,
 BRHIP3017558//11, BRHIP3019956//1, BRHIP3021019//1,
 BRHIP3025795//11, BRHIP3025844//1, BRHIP3027160//1,
 BRHIP3027191//1, BRHIP3028742//2, BRHIP3029530//2,
 5 BRHIP3031733//1, BRHIP3033557//5,
 BRHIP3035222//2, BRHIP3036715//3, BRHIP3036936//1,
 BRHIP3037810//3, BRHIP3039430//4, BRHIP3041587//1,
 BRSSN2004710//1, BRSSN2018218//2, BRSTN2010089//11,
 BRSTN2011688//2, BRSTN2011899//1, BRTHA2000969//2,
 10 BRTHA2003759//3, BRTHA2012189//1, BRTHA2014647//2,
 BRTHA2018304//2, BRTHA2019726//1, BRTHA2019743//2,
 BRTHA2020566//1, BRTHA2020781//1,
 BRTHA2021212//1, BRTHA2021440//1, BRTHA2021450//1,
 BRTHA2022914//2, BRTHA2022968//1, BRTHA2023437//1,
 15 BRTHA2030036//3, BRTHA2031917//1, BRTHA2033469//2,
 BRTHA2033683//7, BRTHA2036055//1, BRTHA2036295//1,
 BRTHA3006593//1, BRTHA3010540//2, BRTHA3010717//4,
 BRTHA3011194//11, BRTHA3011998//3, BRTHA3012265//4,
 BRTHA3013882//3, BRTHA3014835//1,
 20 BRTHA3016616//2, BRTHA3018623//2, BRTHA3028505//1,
 CHONS2001797//1, CHONS2002419//2, COLON2005623//1,
 COLON2005735//10, CTONG2008989//4, CTONG2020582//1,
 CTONG2027150//1, CTONG3001605//5, CTONG3002588//1,
 CTONG3008223//2, FCBBF3012443//1, FEBRA2023498//1,
 25 FEBRA2026977//1, FEHRT2002708//4, FEKID2002231//1,
 FELNG2000720//1, FELNG2001706//1,
 HCHON2009766//12, HSYRA2004550//6, JCMLC2000273//1,
 KIDNE2004531//6, KIDNE2015987//2, KIDNE2017153//1,
 LYMPB1000158//1, LYMPB2002236//12, LYMPB2002478//2,
 30 MESAN2014624//5, N1ESE2000698//1, NETRP2004090//3,
 NETRP2004434//1, NETRP2005282//2, NETRP2005849//2,
 NT2RI3005861//1, NT2RI3009524//1, NT2RP7019682//2,
 NT2RP8001605//2, NT2RP8003787//6,
 NT2RP8008057//1, OCBBF2004478//4, OCBBF2018229//2,
 35 OCBBF2018618//6, OCBBF2036019//2, OCBBF3003745//2,
 OCBBF3007704//1, OCBBF3022123//1, OCBBF3022576//2,

OCBBF3023175//3, OCBBF3023993//3, OCBBF3025475//13,
 OCBBF3025887//1, OCBBF3028001//2, PEBLM2003935//1,
 PEBLM2005615//9, PLACE5000522//2, PLACE6000012//3,
 PLACE6010936//6, PLACE6019674//1,
 5 PLACE7000266//1, PLACE7000707//2, PLACE7003639//3,
 PLACE7008136//2, PLACE7011269//2, PLACE7014247//3,
 PLACE7016321//3, PLACE7016454//2, PUAEN2000684//4,
 SKMUS2008585//2, SMINT2003641//1, SPLEN2007689//2,
 SPLEN2011252//3, SPLEN2031004//1, SPLEN2034551//1,
 10 SPLEN2035615//1, STOMA2004663//1, T1ESE2002665//12,
 TBAES2005361//1, TBAES2007428//2,
 TESOP2008556//1, TESTI2007490//2, TESTI2018335//10,
 TESTI2022323//6, TESTI2024267//9, TESTI2028613//3,
 TESTI2036822//5, TESTI2037085//1, TESTI2037877//1,
 15 TESTI2046188//1, TESTI4001037//2, TESTI4002072//6,
 TESTI4002889//2, TESTI4003602//6, TESTI4004539//8,
 TESTI4004653//9, TESTI4005399//11, TESTI4007671//1,
 TESTI4010544//13, TESTI4010721//6,
 TESTI4013774//2, TESTI4014415//14, TESTI4014932//2,
 20 TESTI4014977//1, TESTI4017647//1, TESTI4017854//2,
 TESTI4019149//1, TESTI4021377//4, TESTI4021569//4,
 TESTI4022158//2, TESTI4023096//9, TESTI4023654//1,
 TESTI4026680//1, TESTI4027170//1, TESTI4028042//2,
 TESTI4031818//1, TESTI4032128//1, TESTI4033177//2,
 25 TESTI4034973//3, TESTI4035989//1,
 TESTI4036012//3, TESTI4037949//2, TESTI4038047//2,
 TESTI4039575//1, TESTI4040559//4, TESTI4041049//2,
 TESTI4043067//1, TESTI4043371//3, TESTI4046073//1,
 TESTI4046450//2, TESTI4047119//11, TESTI4048296//2,
 30 TESTI4048545//1, TESTI4051015//3, TESTI4051858//1,
 TESTI4052219//2, TESTI4052430//1, TESTI4052598//1,
 THYMU3002825//1, THYMU3003007//1,
 THYMU3008935//1, THYMU3009755//2, THYMU3011360//2,
 THYMU3013197//1, THYMU3014173//1, THYMU3015647//9,
 35 THYMU3016518//2, THYMU3018151//2, THYMU3019605//1,
 THYMU3021404//7, THYMU3021586//3, THYMU3022211//2,

THYMU3022528//3, THYMU3022668//1, THYMU3023107//5,
 THYMU3023400//9, THYMU3025313//1, THYMU3025642//2,
 THYMU3026306//1, THYMU3026532//2,
 THYMU3026869//1, THYMU3027540//2, THYMU3031878//4,
 5 THYMU3032032//2, THYMU3033649//2, THYMU3034616//2,
 THYMU3036310//1, THYMU3036934//2, THYMU3038158//1,
 THYMU3040126//3, THYMU3040146//2, THYMU3040172//2,
 THYMU3040746//2, THYMU3040816//2, THYMU3041918//1,
 THYMU3042321//1, THYMU3043688//4, THYMU3043779//2,
 10 THYMU3044188//2, THYMU3047115//7,
 THYMU3047156//3, THYMU3047542//2, THYMU3047760//2,
 TLIVE2008797//1, TRACH3003872//2, TRACH3004747//12,
 TRACH3005274//1, TRACH3005699//1, TRACH3007274//2,
 TRACH3007625//7, TRACH3009008//2, TRACH3009061//6,
 15 TRACH3010382//1, TRACH3011184//1, TRACH3012891//2,
 TRACH3013900//1, TRACH3014063//3, TRACH3015346//1,
 TRACH3016368//1, TRACH3016885//1,
 TRACH3016992//1, TRACH3017409//1, TRACH3018191//2,
 TRACH3018240//1, TRACH3018943//1, TRACH3019370//6,
 20 TRACH3019621//10, TRACH3020930//2, TRACH3022109//3,
 TRACH3023063//3, TRACH3023203//3, TRACH3023945//1,
 TRACH3024081//2, TRACH3024671//2, TRACH3025346//5,
 TRACH3026542//2, TRACH3026650//1, TRACH3027681//2,
 TRACH3029670//2, TRACH3031316//1,
 25 TRACH3031678//8, TRACH3032480//1, TRACH3038399//1,
 TSTOM2002682//1, UTERU3005422//3, UTERU3010029//3,
 UTERU3011092//8, UTERU3011837//1, UTERU3012414//1,
 UTERU3015647//1, UTERU3016273//5, UTERU3017626//6,
 UTERU3022168//1, UTERU3022922//2, UTERU3023413//1
 30 Deduced amino acid sequences of following 14 clones were
 also detected to have the transmembrane domains by SOSUI.
 BRAWH3013197//6, BRAWH3028645//7, BRAWH3046240//7,
 BRTHA3024233//3, PROST2010326//8, TBAES2004105//1,
 TBAES2007379//1, TBAES2007481//1, TESTI2043585//8,
 35 THYMU3024602//8, THYMU3044175//2, THYMU3046350//9,
 TLIVE2007192//2, TRACH3021066//2

The 796 clones whose deduced amino acid sequences were detected to have functional domains with Pfam are as follows. The search result is indicated as "Clone Name//Functional Domain Name". When the clone has Multiple Hit Functional Domains, they are listed and demarcated by a double slash mark (/). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

- 3NB692004045//Sodium Bile acid symporter family// FecCD transport family
- 10 ADIPS2000069//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- ASTRO2016114//Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 15 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- BEAST2000981//PA domain// Zinc finger, C3HC4 type (RING finger)// PHD-finger
- 20 BLADE2001031//Thrombospondin type 1 domain
- BLADE2002310//RhoGAP domain
- BLADE2008809//PH domain
- BRACE1000475//Enoyl-CoA hydratase/isomerase family
- BRACE2003628//NADH-Ubiquinone oxidoreductase (complex I), chain
- 25 5 C-terminus
- BRACE2010336//TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain
- BRACE2012528//alpha/beta hydrolase fold
- BRACE2012625//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
- 30 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- BRACE2013009//EF hand
- BRACE2013132//Adenosine/AMP deaminase
- 35 BRACE2016896//tRNA synthetases class II (F)// tRNA synthetases class II (F)// tRNA synthetases class II (D, K and N)

- BRACE2017397//von Willebrand factor type A domain
 BRACE2017872//PWWP domain
 BRACE2019348//Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRACE2023744//Translationally controlled tumor protein
 5 BRACE2034434//Protein of unknown function
 BRACE2035120//Inositol polyphosphate phosphatase family,
 catalytic domain
 BRACE2042541//Ank repeat// Ank repeat// Glutathione S-
 transferases.
 10 BRACE2046976//Collagen triple helix repeat (20 copies)
 BRACE2047975//Eukaryotic protein kinase domain
 BRACE3001973//EGF-like domain// Laminin G domain// EGF-like
 domain// EGF-like domain// EGF-like domain
 BRACE3002264//GNS1/SUR4 family// Ion transport protein// Ion
 15 transport protein
 BRACE3002344//WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 PQQ enzyme repeat// WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
 20 BRACE3002756//SAM domain (Sterile alpha motif)
 BRACE3003866//Src homology domain 2
 BRACE3004767//PH domain
 BRACE3005903//K-box region// TSC-22/dip/bun family
 BRACE3009392//Aminotransferases class-III pyridoxal-phosphate//
 25 Sodium:dicarboxylate symporter family
 BRACE3013418//Ank repeat// Ank repeat// ZU5 domain// Death
 domain// TGF-beta propeptide// Fatty acid desaturase//
 Isocitrate lyase
 BRACE3013874//Leucine rich repeat C-terminal domain//
 30 Immunoglobulin domain// Fibronectin type III domain
 BRACE3014523//Wiskott Aldrich syndrome homology region 2
 BRACE3015898//PI3-kinase family, ras-binding domain
 BRACE3017253//Adenylate kinase// Transferrin
 BRACE3019570//Troponin
 35 BRACE3019941//TPR Domain// TPR Domain// DNA-dependent RNA
 polymerase// TPR Domain// TPR Domain// TPR Domain// 7-fold

repeat in Clathrin and VPS// TPR Domain// TPR Domain// TPR
 Domain// TPR Domain
 BRACE3022303//BRCA1 C Terminus (BRCT) domain// BRCA1 C Terminus
 (BRCT) domain
 5 BRACE3022340//Troponin
 BRACE3024444//Copper/zinc superoxide dismutase (SODC)
 BRACE3024879//7 transmembrane receptor (Secretin family)
 BRACE3025719//Zinc finger, C3HC4 type (RING finger)//
 Filamin/ABP280 repeat.// NHL repeat// NHL repeat// NHL repeat//
 10 NHL repeat// Squash family of serine protease inhibitors
 BRACE3026345//Insulin/IGF/Relaxin family
 BRACE3026844//KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc
 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2
 type
 20 BRACE3026947//FYVE zinc finger
 BRACE3029021//Zinc finger, C2H2 type
 BRACE3031315//Serine hydroxymethyltransferase// UBA domain
 BRACE3031372//D-isomer specific 2-hydroxyacid dehydrogenases
 BRACE3031743//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 25 domain)
 BRACE3032385//Ion transport protein
 BRACE3032537//Luteovirus (ORF3) RNA-directed RNA-polymerase
 BRACE3033525//Prolyl oligopeptidase family
 BRACE3034183//Zinc finger, C2H2 type// PHD-finger// Zinc finger,
 30 C2H2 type// Plant PEC family metallothionein// Transcription
 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// FYVE zinc finger// Zinc finger,
 C2H2 type// RNA polymerases M/15 Kd subunits// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc
 35 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc

finger, C2H2 type
 BRACE3034964//alpha/beta hydrolase fold
 BRACE3036283//DnaJ domain
 BRACE3039288//Viral RNA dependent RNA polymerase
 5 BRACE3039358//Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine rich repeat C-terminal domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 BRACE3039378//Pentaxin family// Receptor family ligand binding
 region// 7 transmembrane receptor (metabotropic glutamate
 10 family)
 BRACE3039454//Aminotransferases class-III pyridoxal-phosphate
 BRACE3040239//Zinc finger, C3HC4 type (RING finger)
 BRACE3040644//Low-density lipoprotein receptor domain class A//
 EB module// Low-density lipoprotein receptor domain class A//
 15 CUB domain// Low-density lipoprotein receptor domain class A//
 Low-density lipoprotein receptor domain class A
 BRACE3041059//Ubiquitin carboxyl-terminal hydrolases family 2//
 Ubiquitin carboxyl-terminal hydrolase family 2
 BRACE3041162//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 20 PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Putative zinc
 finger in N-recognin
 BRACE3042046//RhoGEF domain// PH domain
 BRACE3042409//AMP-binding enzyme
 25 BRACE3042432//7 transmembrane receptor (Secretin family)
 BRACE3043597//KOW motif
 BRACE3044172//Phosphatidylinositol 3- and 4-kinases
 BRACE3045424//PH domain
 BRACE3046466//EGF-like domain// EGF-like domain// Laminin G
 30 domain// Laminin G domain// EGF-like domain// Laminin G domain//
 EGF-like domain// Laminin G domain// Laminin G domain// EGF-like
 domain// EGF-like domain// Laminin EGF-like (Domains III and
 V)// EB module// EGF-like domain// EGF-like domain
 BRACE3046491//PDZ domain (Also known as DHR or GLGF).// PDZ
 35 domain (Also known as DHR or GLGF).// PDZ domain (Also known as
 DHR or GLGF).// SH3 domain// Guanylate kinase

- BRACE3047482//Zinc finger, C3HC4 type (RING finger)// Zinc finger, C3HC4 type (RING finger)// B-box zinc finger.// CONSTANS family zinc finger// B-box zinc finger.// Fibronectin type III domain// SPRY domain
- 5 BRACE3048615//Leucine Rich Repeat// Leucine Rich Repeat
BRACE3049714//Dihydroneopterin aldolase
BRACE3050270//Reverse transcriptase (RNA-dependent DNA polymerase)
BRACE3050504//Ion transport protein
- 10 BRACE3051621//Latrophilin/CL-1-like GPS domain// PLAT/LH2 domain// Regulator of G protein signaling domain
BRACE3051819//Myosin head (motor domain)// IQ calmodulin-binding motif// IQ calmodulin-binding motif// Myosin tail// KE2 family protein// Myosin tail// lactate/malate dehydrogenase//
- 15 Troponin// Myosin tail
BRACE3052321//SH3 domain
BRACE3052410//Viral methyltransferase
BRACE3052595//C2 domain
BRALZ2010842//Mitochondrial carrier proteins
- 20 BRALZ2013621//KH domain
BRAMY2031516//wnt family of developmental signaling proteins
BRAMY2040915//Immunoglobulin domain
BRAMY2041347//Mov34/MPN/PAD-1 family
BRAMY2041384//Annexin// Annexin// Annexin// Annexin// Annexin//
- 25 Annexin
BRAMY2046537//PMP-22/EMP/MP20/Claudin family
BRAMY3000692//Zinc finger, C2H2 type// Zinc finger, C2H2 type
BRAMY3002886//Domain of unknown function// CBS domain// CBS domain
- 30 BRAMY3004126//Transmembrane 4 family// 7 transmembrane receptor (rhodopsin family)
BRAMY3005184//ZU5 domain// Death domain
BRAMY3007078//Inositol monophosphatase family// PHD-finger// PHD-finger
- 35 BRAMY3009491//Phosphatidylinositol 3- and 4-kinases
BRAMY3010321//SAM domain (Sterile alpha motif)// PH domain// PH

domain// Putative GTP-ase activating protein for Arf
 BRAMY3011501//SAP domain// SPRY domain
 BRAMY3011581//Prokaryotic DNA topoisomerase// Topoisomerase DNA
 binding C4 zinc finger// PHD-finger// Zinc finger, CCHC class
 5 BRAMY3014027//KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 10 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type
 BRAMY3014613//RhoGAP domain// haloacid dehalogenase-like
 15 hydrolase
 BRAMY3015086//FERM domain (Band 4.1 family)
 BRAMY3015547//RhoGEF domain
 BRAMY3015549//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 20 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain
 BRAMY3017920//RhoGEF domain// PH domain// RhoGAP domain
 BRAMY3018754//Protein of unknown function// Domain of unknown
 25 function
 BRAMY4000915//Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Glutamine amidotransferases class-II// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank
 30 repeat// Hantavirus nucleocapsid protein// Ank repeat// Ank
 repeat
 BRAMY4000962//Tudor domain
 BRAMY4001652//Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank
 35 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ribosomal protein L34// Ank repeat// Ank repeat// Ank

repeat// Uncharacterized protein family UPF0028
 BRAMY4002575//Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRAWH2000256//Progesterone receptor// Cytochrome c oxidase
 5 subunit III// Sulfate transporter family
 BRAWH2002333//3'5'-cyclic nucleotide phosphodiesterase
 BRAWH2011796//S-100/ICaBP type calcium binding domain// EF hand
 BRAWH2011812//Syndecan domain// BNR repeat// BNR repeat// BNR
 repeat// BNR repeat// BNR repeat// PKD domain
 10 BRAWH2012866//C2 domain// C2 domain
 BRAWH2014053//Sigma-54 transcription factors// ATPases
 associated with various cellular activities (AAA)
 BRAWH2016209//Zinc finger, C3HC4 type (RING finger)// PHD-finger
 BRAWH2016223//TPR Domain
 15 BRAWH2016785//Pyridine nucleotide-disulphide oxidoreductase
 BRAWH3000446//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 BRAWH3001783//Cadherin domain// Cadherin domain// Cadherin
 20 domain// Cadherin domain// Cadherin domain
 BRAWH3003573//EF hand// EF hand// EF hand
 BRAWH3005886//Rubredoxin// PHD-finger
 BRAWH3008167//Sushi domain (SCR repeat)// CUB domain// Sushi
 domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)//
 25 CUB domain// Sushi domain (SCR repeat)// CUB domain
 BRAWH3009961//PHD-finger// Glycophorin A// PDZ domain (Also
 known as DHR or GLGF).// C2 domain// C2 domain
 BRAWH3010657//Ubiquitin carboxyl-terminal hydrolases family 2//
 Ubiquitin carboxyl-terminal hydrolase family 2
 30 BRAWH3011331//Disintegrin
 BRAWH3011577//KRAB box
 BRAWH3011623//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 BRAWH3013009//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//

- Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Putative zinc finger in N-recognin// Zinc finger, C2H2 type// DM DNA binding domain// Zinc finger, C2H2 type
- 5 BRAWH3013264//SNF2 and others N-terminal domain// SNF2 and others N-terminal domain// TPR Domain// 3C cysteine protease (picornain 3C)// Zinc finger, C3HC4 type (RING finger)// Plant PEC family metallothionein// Helicases conserved C-terminal domain
- 10 BRAWH3014609//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
- 15 Leucine rich repeat C-terminal domain
BRAWH3015175//Xylose isomerase// Intermediate filament proteins// Helix-loop-helix DNA-binding domain// ATP synthase Alpha chain, C terminal
BRAWH3015610//TFIIE beta subunit core domain
- 20 BRAWH3017180//Phorbol esters/diacylglycerol binding domain (C1 domain)// Diacylglycerol kinase catalytic domain (presumed)// Diacylglycerol kinase accessory domain (presumed)// Ank repeat// Ank repeat
BRAWH3017259//Carboxylesterases// Syntaxin// SAM domain (Sterile
- 25 alpha motif)
BRAWH3017260//Pancreatic hormone peptides
BRAWH3017477//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
BRAWH3018063//Rap/ran-GAP
- 30 BRAWH3018548//Intermediate filament proteins// Vinculin family
BRAWH3019026//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Protein phosphatase 2A regulatory subunit PR55// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
- 35 BRAWH3021574//Wiskott Aldrich syndrome homology region 2
BRAWH3021580//Intermediate filament proteins// Zinc finger, CCHC

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class
BRAWH3021724//Transglutaminase-like superfamily
BRAWH3022347//Leucine Rich Repeat
BRAWH3022431//FGGY family of carbohydrate kinases
5  BRAWH3022651//PHD-finger// Zn-finger in ubiquitin-hydrolases and
   other proteins
BRAWH3022719//Eukaryotic initiation factor 4E
BRAWH3023156//Neurotransmitter-gated ion-channel
BRAWH3023415//Glycosyl hydrolase family 47
10  BRAWH3024186//Fibronectin type III domain// Protein-tyrosine
   phosphatase// Dual specificity phosphatase, catalytic domain//
   Protein-tyrosine phosphatase
BRAWH3024231//TPR Domain// TPR Domain// TPR Domain
BRAWH3024506//I/LWEQ domain
15  BRAWH3025157//Ank repeat// Ank repeat// Ank repeat// BTB/POZ
   domain// K+ channel tetramerisation domain
BRAWH3026349//PX domain
BRAWH3026938//PDZ domain (Also known as DHR or GLGF).
BRAWH3027440//TPR Domain// TPR Domain// TPR Domain// TPR
20  Domain// PPR repeat
BRAWH3027533//AN1-like Zinc finger// PHD-finger// FYVE zinc
   finger
BRAWH3027574//TBC domain// EF hand
BRAWH3027607//DNA binding domain with preference for A/T rich
25  regions
BRAWH3027806//WD domain, G-beta repeat// WD domain, G-beta
   repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
   Arenavirus nucleocapsid protein// WD domain, G-beta repeat// WD
   domain, G-beta repeat
30  BRAWH3027880//Integral membrane protein// AN1-like Zinc finger//
   DHHC zinc finger domain
BRAWH3028796//Zinc finger C-x8-C-x5-C-x3-H type (and similar).//
   Zinc finger C-x8-C-x5-C-x3-H type (and similar).// Zinc finger
   C-x8-C-x5-C-x3-H type (and similar).// Zinc finger, C3HC4 type
35  (RING finger)// Integrase Zinc binding domain// Zinc finger C-
   x8-C-x5-C-x3-H type (and similar).// Protein phosphatase 2A

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regulatory B subunit (B56 family)
 BRAWH3029385//PH domain// Dynamin GTPase effector domain
 BRAWH3029806//Copper/zinc superoxide dismutase (SODC)//
 Adenylate and Guanylate cyclase catalytic domain// NADH-
 5 ubiquinone oxidoreductase chain 4, amino terminus// Endothelin
 family
 BRAWH3030772//Ank repeat// Ank repeat// Ank repeat
 BRAWH3030910//SAM domain (Sterile alpha motif)
 BRAWH3031342//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Putative zinc finger in N-recogin//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 factor S-II (TFIIS)// Src homology domain 2// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc
 finger, C2H2 type
 BRAWH3031710//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 20 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 BRAWH3032298//EGF-like domain// EGF-like domain// EGF-like
 domain// EB module// EGF-like domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 25 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibrinogen beta and gamma chains, C-terminal globular
 domain
 30 BRAWH3032340//RhoGEF domain// PH domain// Ezrin/radixin/moesin
 family
 BRAWH3032571//PHD-finger// von Willebrand factor type C domain//
 PHD-finger// 'chromo' (CHRromatin Organization MODifier)
 domain// 'chromo' (CHRromatin Organization MODifier) domain//
 35 DEAD/DEAH box helicase// SNF2 and others N-terminal domain//
 Helicases conserved C-terminal domain

BRAWH3033448//TPR Domain// TPR Domain
 BRAWH3033513//Thiolase
 BRAWH3034668//Ubiquitin carboxyl-terminal hydrolases family 2//
 E7 protein, Early protein// Ubiquitin carboxyl-terminal
 5 hydrolase family 2
 BRAWH3034743//ATP synthase (E/31 kDa) subunit//
 Ezrin/radixin/moesin family
 BRAWH3034775//SAP domain// SPRY domain
 BRAWH3035403//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 10 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 BRAWH3035914//TBC domain
 BRAWH3035936//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 20 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 BRAWH3036247//BTB/POZ domain// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 25 type// Phorbol esters/diacylglycerol binding domain (C1
 domain)// Zinc finger, C2H2 type// Ribosomal protein L31// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 BRAWH3036270//Atrial natriuretic peptide
 30 BRAWH3036334//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//

Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 BRAWH3037265//SURF4 family
 BRAWH3037428//ADP-ribosylation factor family// Ras family
 5 BRAWH3037979//wnt family of developmental signaling proteins//
 Ubiquitin carboxyl-terminal hydrolases family 2// Ubiquitin
 carboxyl-terminal hydrolase family 2
 BRAWH3038055//Spectrin repeat// Myb-like DNA-binding domain//
 Spectrin repeat// 7-fold repeat in Clathrin and VPS// Spectrin
 10 repeat// Spectrin repeat// Spectrin repeat// Spectrin repeat//
 Spectrin repeat
 BRAWH3038252//Formin Homology 2 Domain
 BRAWH3038324//Dehydrins
 BRAWH3038827//Kelch motif// Kelch motif// Kelch motif// Kelch
 15 motif// BTB/POZ domain// BTB/POZ domain
 BRAWH3041556//Tetrahydrofolate dehydrogenase/cyclohydrolase//
 Formate--tetrahydrofolate ligase
 BRAWH3041928//Wilm's tumour protein
 BRAWH3042438//'Paired box' domain// EF hand// Phorbol
 20 esters/diacylglycerol binding domain (C1 domain)
 BRAWH3042568//Homeobox domain
 BRAWH3042772//Cation efflux family
 BRAWH3042787//Gag P30 core shell protein// Zinc finger, CCHC
 class
 25 BRAWH3043295//Inorganic pyrophosphatase
 BRAWH3044122//C2 domain// Sigma-70 factor
 BRAWH3044151//Thrombospondin type 1 domain// Thrombospondin type
 1 domain// Thrombospondin type 1 domain// Keratin, high sulfur
 B2 protein// Thrombospondin type 1 domain
 30 BRAWH3044985//Phosphotriesterase family
 BRAWH3045118//DnaJ domain
 BRAWH3046424//Histone deacetylase family
 BRAWH3047692//Shikimate kinase// ATPases associated with various
 cellular activities (AAA)
 35 BRAWH3048374//Sushi domain (SCR repeat)// Sushi domain (SCR
 repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR

repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR
 repeat)// Sushi domain (SCR repeat)// Keratin, high sulfur B2
 protein// Sushi domain (SCR repeat)
 BRAWH3048724//Subtilase family
 5 BRAWH3049544//Glycosyl transferases// Similarity to lectin
 domain of ricin beta-chain, 3 copies.
 BRCAN2000923//ADP-ribosylation factor family// Ras family
 BRCAN2002892//ADP-ribosylation factor family// Ras family
 BRCAN2003269//ABC transporter
 10 BRCAN2003814//Phosphatidylinositol-specific phospholipase C, X
 domain
 BRCAN2006051//Peptidase family M41
 BRCAN2010665//PDZ domain (Also known as DHR or GLGF).// PDZ
 domain (Also known as DHR or GLGF).// PDZ domain (Also known as
 15 DHR or GLGF).
 BRCAN2015402//Cytochrome P450
 BRCAN2019907//EF hand
 BRCAN2020234//Lipocalin / cytosolic fatty-acid binding protein
 family
 20 BRCAN2020331//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 BRCAN2021325//Zinc carboxypeptidase// Zinc carboxypeptidase
 25 BRCAN2021452//Zinc finger, CCHC class// Zinc finger, CCHC class
 BRCAN2021718//Ribosomal protein L10
 BRCAN2022126//IstB-like ATP binding protein// Receptor family
 ligand binding region// Bacterial extracellular solute-binding
 proteins, family 3// Ligand-gated ion channel
 30 BRCAN2025093//Ank repeat// Flagellar FliJ protein// Ank repeat
 BRCOC2001355//GTP1/OBG family// Phosphoribulokinase//
 Adenylylsulfate kinase
 BRCOC2006164//ATP synthase subunit C// Nucleoside transporter//
 Sugar (and other) transporter// Influenza RNA-dependent RNA
 35 polymerase subunit PA
 BRCOC2006639//Leucine Rich Repeat// Leucine Rich Repeat//

Leucine Rich Repeat// Leucine Rich Repeat
 BRCOC2012386//KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 5 finger, C2H2 type// Zinc finger, C2H2 type
 BRHIP2008756//MAS20 protein import receptor// BRCA1 C Terminus
 (BRCT) domain
 BRHIP2013958//Domain of unknown function// MSP (Major sperm
 protein) domain
 10 BRHIP2026346//Formin Homology 2 Domain
 BRHIP2027077//Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRHIP2027563//Kelch motif
 BRHIP2029663//TPR Domain// Zinc finger, C3HC4 type (RING
 finger)// ATP-dependent protease La (LON) domain
 15 BRHIP3000859//Wilm's tumour protein
 BRHIP3001481//Protein-tyrosine phosphatase
 BRHIP3001878//POT family
 BRHIP3002000//Peptidase family M20/M25/M40// Sugar (and other)
 transporter
 20 BRHIP3002114//Mandelate racemase / muconate lactonizing enzyme
 family
 BRHIP3002141//DNA polymerase (viral) C-terminal domain
 BRHIP3003063//cAMP phosphodiesterases class-II// Vinculin family
 BRHIP3003126//HECT-domain (ubiquitin-transferase).
 25 BRHIP3003306//Uncharacterized protein family// Rap/ran-GAP
 BRHIP3003340//Actin
 BRHIP3003795//Cytochrome P450
 BRHIP3004710//TPR Domain// TPR Domain// TPR Domain
 BRHIP3004725//tRNA synthetases class I (C)
 30 BRHIP3005037//BAH domain// ELM2 domain// Myb-like DNA-binding
 domain// GATA zinc finger
 BRHIP3005142//Adaptin N terminal region
 BRHIP3005231//TPR Domain// TPR Domain
 BRHIP3005307//Glutathione S-transferases.// Uncharacterized
 35 protein family UPF0028
 BRHIP3005673//Glutathione S-transferases.

BRHIP3005944//Scavenger receptor cysteine-rich domain//
 Scavenger receptor cysteine-rich domain
 BRHIP3006294//SH3 domain// RhoGAP domain
 BRHIP3006449//Armadillo/beta-catenin-like repeats//
 5 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// Armadillo/beta-catenin-like repeats//
 Armadillo/beta-catenin-like repeats
 BRHIP3006786//Sec7 domain
 BRHIP3007195//Type I restriction modification DNA specificity
 10 domain// E1-E2 ATPase// E1-E2 ATPase// Neuraxin and MAP1B
 proteins// E1-E2 ATPase// Cof family
 BRHIP3007223//Ubiquitin carboxyl-terminal hydrolases family 2//
 Ubiquitin carboxyl-terminal hydrolase family 2
 BRHIP3007424//wnt family of developmental signaling proteins
 15 BRHIP3007609//PHD-finger
 BRHIP3008320//Transmembrane region cyclic Nucleotide Gated
 Channel
 BRHIP3009753//CUB domain// Low-density lipoprotein receptor
 domain class A
 20 BRHIP3010289//Delta serrate ligand// Kelch motif// Kelch motif//
 Plexin repeat// Plexin repeat// Lectin C-type domain// Plexin
 repeat// Plexin repeat// Laminin EGF-like (Domains III and V)//
 Keratin, high sulfur B2 protein// Laminin EGF-like (Domains III
 and V)
 25 BRHIP3011082//HECT-domain (ubiquitin-transferase).
 BRHIP3011460//RhoGEF domain// PH domain// SH3 domain
 BRHIP3011567//Dihydropyridine sensitive L-type calcium channel
 (Beta subunit)// Dihydropyridine sensitive L-type calcium
 channel (Beta subunit)
 30 BRHIP3012289//Flavin containing amine oxidase
 BRHIP3012736//Collagen triple helix repeat (20 copies)
 BRHIP3014675//Ank repeat// Ank repeat// Ank repeat// BTB/POZ
 domain// K⁺ channel tetramerisation domain
 BRHIP3016032//Integral membrane protein// Divalent cation
 35 transporter// TPR Domain// TPR Domain// TPR Domain
 BRHIP3017109//Src homology domain 2

BRHIP3017256//LIM domain containing proteins// AN1-like Zinc
finger

BRHIP3017558//eubacterial secY protein// FecCD transport
family// Domain of unknown function// Sugar (and other)

5 transporter// Sodium:galactoside symporter family//
Monocarboxylate transporter

BRHIP3019643//Biopterin-dependent aromatic amino acid
hydroxylase

BRHIP3019824//Prokaryotic transcription elongation factor,
10 GreA/GreB

BRHIP3020733//Keratin, high sulfur B2 protein

BRHIP3021019//Protein-tyrosine phosphatase// Dual specificity
phosphatase, catalytic domain

BRHIP3025795//Sugar (and other) transporter// Protein of unknown
15 function// Sodium:galactoside symporter family// Herpesvirus
glycoprotein M// Monocarboxylate transporter

BRHIP3027191//Hsp70 protein

BRHIP3027651//PHD-finger// PHD-finger

BRHIP3028246//CXXC zinc finger// PHD-finger// Beta type Zein

20 BRHIP3028570//PH domain// Fibroblast growth factor

BRHIP3029409//NTR/C345C module

BRHIP3030230//Pentaxin family

BRHIP3032374//Glutathione S-transferases.// Uncharacterized
protein family UPF0028

25 BRHIP3033557//Pyridoxamine 5'-phosphate oxidase// Ligand-gated
ion channel

BRHIP3033734//Keratin, high sulfur B2 protein

BRHIP3035006//Sialyltransferase family

BRHIP3036371//Immunoglobulin domain// Kunitz/Bovine pancreatic

30 trypsin inhibitor domain// Kunitz/Bovine pancreatic trypsin
inhibitor domain

BRHIP3036715//Class I Histocompatibility antigen, domains alpha
1 and 2// Immunoglobulin domain

BRHIP3036936//Fibronectin type III domain

35 BRHIP3037543//Eukaryotic protein kinase domain

BRHIP3038030//Pyridine nucleotide-disulphide oxidoreductase//

Phytoene dehydrogenase related enzyme
 BRHIP3038735//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain
 BRHIP3039509//Notch (DSL) domain// Amiloride-sensitive sodium
 5 channel
 BRHIP3039592//Zinc finger, C3HC4 type (RING finger)
 BRHIP3041587//Eukaryotic protein kinase domain
 BRSSN2004710//3'5'-cyclic nucleotide phosphodiesterase
 BRSSN2011843//bZIP transcription factor// RNA polymerase alpha
 10 subunit
 BRSSN2015497//Tudor domain
 BRSTN2006638//EF hand// EF hand// Pancreatic hormone peptides
 BRSTN2010089//Cell cycle protein// 7 transmembrane receptor
 (Secretin family)
 15 BRSTN2011961//Thioredoxin
 BRSTN2012069//Elongation factor Tu family
 BRSTN2016918//Transposase// Ezrin/radixin/moesin family//
 Intermediate filament proteins
 BRTHA2001304//Exonuclease
 20 BRTHA2005448//Calpain family cysteine protease// Calpain large
 subunit, domain III// EF hand
 BRTHA2019726//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 BRTHA2020400//Immunoglobulin domain
 25 BRTHA2020721//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 BRTHA2020910//Tubulin/FtsZ family
 BRTHA2025869//Intermediate filament proteins// Intermediate
 filament proteins
 30 BRTHA2026290//Guanine nucleotide exchange factor for Ras-like
 GTPases; N-terminal motif// Initiator RepB.protein// RasGEF
 domain
 BRTHA2026311//Thioredoxin// Thioredoxin
 BRTHA2027250//C2 domain// C2 domain
 35 BRTHA2030036//Lipase
 BRTHA2031917//Fibronectin type III domain// Photosynthetic

- reaction center protein
 BRTHA2033683//E1-E2 ATPase
 BRTHA2035743//Serine hydroxymethyltransferase// UBA domain
 BRTHA2036295//Helper component proteinase
- 5 BRTHA2037247//Reverse transcriptase (RNA-dependent DNA polymerase)
 BRTHA2038345//Ank repeat// Ank repeat// Ank repeat
 BRTHA3000456//Zinc finger, C2H2 type// DM DNA binding domain//
 Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)//
- 10 Zinc finger, C2H2 type// Putative zinc finger in N-recognin//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
- 15 BRTHA3003225//Zinc finger, C3HC4 type (RING finger)// PHD-finger
 BRTHA3003736//DEAD/DEAH box helicase// Helicases conserved C-terminal domain
 BRTHA3010135//Protein-tyrosine phosphatase// Protein-tyrosine phosphatase
- 20 BRTHA3010212//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 25 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
- BRTHA3011187//EF hand
- 30 BRTHA3011194//Voltage gated chloride channels// CBS domain
 BRTHA3011361//Calponin homology (CH) domain// LIM domain containing proteins
 BRTHA3012265//Sulfate transporter family// Ribosomal protein S3, C-terminal domain.
- 35 BRTHA3014000//Birnavirus VP3 protein// Zinc finger, C2H2 type// ELM2 domain// Myb-like DNA-binding domain// Zinc finger, C2H2

type// Zinc finger, C2H2 type
 BRTHA3014547//Adenylate kinase// Viral (Superfamily 1) RNA
 helicase// Arsenical pump membrane protein// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Dehydrogenase E1
 5 component// Ank repeat// Shikimate / quinate 5-dehydrogenase//
 Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//
 Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//
 Ank repeat
 BRTHA3017791//Lectin (probable mannose binding)
 10 BRTHA3018409//Wilm's tumour protein
 BRTHA3020771//PH domain
 BRTHA3021708//PH domain
 BRTHA3021786//Protein prenyltransferase alpha subunit repeat
 BRTHA3021971//Putative peptidoglycan binding domain
 15 BRTHA3023403//Phosphatidylinositol-specific phospholipase C, X
 domain// Phosphatidylinositol-specific phospholipase C, X
 domain// C2 domain
 BRTHA3025073//Calponin homology (CH) domain
 BRTHA3026161//Adenosine-deaminase (editase) domain
 20 BRTHA3026916//Guanine nucleotide exchange factor for Ras-like
 GTPases; N-terminal motif// RasGEF domain// Ras association
 (RalGDS/AF-6) domain
 BRTHA3027171//Scorpion short toxins
 BRTHA3027638//Matrix protein (MA), p15
 25 BRTHA3028339//Zn-finger in Ran binding protein and others.
 CERVX2000968//Immunoglobulin domain
 CHONS2000797//T-box
 CHONS2001287//Insulin-like growth factor binding proteins//
 Thyroglobulin type-1 repeat
 30 CHONS2001834//Plexin repeat
 CHONS2002829//F5/8 type C domain// Zinc carboxypeptidase// Zinc
 carboxypeptidase// Zinc carboxypeptidase
 COLON2004351//Galactosyltransferase
 COLON2005735//CbiM// Ammonium Transporter Family
 35 CTONG2003517//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)

CTONG2006235//Zn-finger in ubiquitin-hydrolases and other proteins

CTONG2008989//Connexin

CTONG2009570//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//

5 CTONG2010330//Lysophospholipase catalytic domain

CTONG2011801//BTB/POZ domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc

10 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG2020582//AMP-binding enzyme

CTONG2026987//Reverse transcriptase (RNA-dependent DNA

15 polymerase)

D9OST2003106//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

D9OST2004417//Ribosomal protein L13e

20 DFNES2011221//Rotavirus NS26

ERLTF2002178//Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif

ERLTF2002369//PH domain// RhoGAP domain// Tropomyosins

FCBBF3001018//HMGL-like

25 FCBBF3012443//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat C-terminal domain

FCBBF3020030//B-box zinc finger.// B-box zinc finger.// Putative

30 zinc finger in N-recognin

FCBBF3021191//Protein phosphatase 2C// Protein phosphatase 2C

FCBBF3024911//PWWP domain

FCBBF5000384//BAF60b domain of the SWIB complex

FEBRA2000805//Uncharacterized protein family UPF0054

35 FEBRA2002260//CXXC zinc finger

FEBRA2013570//Dehydrogenase E1 component

FEBRA2023498//Leucine rich repeat N-terminal domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 FEBRA2026582//PPIC-type PPIASE domain.
 FEBRA2028457//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 5 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 FEHRT2002708//DNA gyrase/topoisomerase IV, subunit A
 10 FEKID2001001//SH3 domain// WW domain// WW domain// PH domain
 FEKID2002493//wnt family of developmental signaling proteins
 FEKID2002637//Ser/Thr protein phosphatase
 FELNG2000720//Immunoglobulin domain// Immunoglobulin domain
 FELNG2001953//Src homology domain 2
 15 HCASM2008154//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// Zn-finger in Ran binding protein and others.
 HCHON2009766//eIF4-gamma/eIF5/eIF2-epsilon
 HHDP2008185//Helper component proteinase// Site-specific
 recombinases
 20 HSYRA2004550//E1-E2 ATPase// E1-E2 ATPase
 HSYRA2007338//Fibronectin type III domain
 JCMLC2000273//Lysosome-associated membrane glycoprotein (Lamp)//
 Integrin alpha cytoplasmic region
 JCMLC2002751//von Willebrand factor type D domain// Plant PEC
 25 family metallothionein// Trypsin Inhibitor like cysteine rich
 domain// von Willebrand factor type C domain// von Willebrand
 factor type D domain
 KIDNE2004531//Prion protein// Integral membrane protein//
 Cytochrome c oxidase subunit III// Uncharacterized protein
 30 family
 KIDNE2010049//FGGY family of carbohydrate kinases// FGGY family
 of carbohydrate kinases
 KIDNE2015987//EGF-like domain// Keratin, high sulfur B2
 protein// Zona pellucida-like domain
 35 KIDNE2018268//Zinc finger, C2H2 type
 LYMPB2002236//ABC 3 transport family// CbiM// NADH-ubiquinone

oxidoreductase chain 4, amino terminus// UDP-glucuronosyl and
 UDP-glucosyl transferases
 LYMPB2002344//TBC domain
 LYMPB2002458//Fibronectin type III domain// Fibronectin type III
 5 domain// Fibrinogen beta and gamma chains, C-terminal globular
 domain
 N1ESE2000698//WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain,
 10 G-beta repeat// WD domain, G-beta repeat
 NETRP2003103//Zinc finger, C3HC4 type (RING finger)// PHD-finger
 NETRP2003448//ADP-ribosylation factor family// Ras family
 NETRP2004017//Histone-like transcription factor (CBF/NF-Y) and
 archaeal histone// 2S seed storage family
 15 NT2RI2004818//Phosphatidylinositol-specific phospholipase C, X
 domain// Phosphatidylinositol-specific phospholipase C, X
 domain// C2 domain// Fes/CIP4 homology domain
 NT2RI3001573//Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat
 20 NT2RI3001967//Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Glutathione S-transferases// SAM domain (Sterile alpha
 motif)
 NT2RI3005923//Cadherin domain// Cadherin domain// Cadherin
 domain// Cadherin domain// Cadherin domain// Cadherin domain//
 25 Cadherin domain// Cadherin domain// Cadherin domain// Cadherin
 domain// Cadherin domain
 NT2RI3009480//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 NT2RI3009524//EGF-like domain// EGF-like domain// EGF-like
 30 domain// EGF-like domain// EGF-like domain// EGF-like domain//
 EGF-like domain// EGF-like domain// Metallothionein// EGF-like
 domain// Laminin G domain// Laminin G domain// EGF-like domain//
 Laminin G domain// EGF-like domain// Laminin G domain// Laminin
 G domain// EGF-like domain// EGF-like domain
 35 NT2RP7007387//Armadillo/beta-catenin-like repeats// picornavirus
 capsid protein

- OCBBF2000831//WAP-type (Whey Acidic Protein) 'four-disulfide core'// Kazal-type serine protease inhibitor domain// Immunoglobulin domain// Kunitz/Bovine pancreatic trypsin inhibitor domain// Kunitz/Bovine pancreatic trypsin inhibitor domain// Furin-like cysteine-rich region// Respiratory-chain NADH dehydrogenase, 49 Kd subunit// NTR/C345C module
- 5 OCBBF2003518//Transient receptor// Transient receptor
OCBBF2004478//Trypanosome variant surface glycoprotein// 7 transmembrane receptor (Secretin family)
- 10 OCBBF2007039//Reprolysin family propeptide// Reprolysin (M12B) family zinc metalloprotease// Thrombospondin type 1 domain// EB module
OCBBF2009536//Amiloride-sensitive sodium channel
OCBBF2014745//Zinc finger, C2H2 type// Zinc finger, C2H2 type
- 15 OCBBF2016928//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- 20 OCBBF2018618//7 transmembrane receptor (Secretin family)// 7 transmembrane receptor (rhodopsin family)
OCBBF2024589//Glutamine amidotransferases class-II// Dihydroorotase-like
OCBBF2030927//Neuregulin family// von Willebrand factor type A
- 25 domain// EGF-like domain// Response regulator receiver domain// von Willebrand factor type A domain// von Willebrand factor type A domain
OCBBF3001202//DENN (AEX-3) domain
OCBBF3001333//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 30 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- OCBBF3001616//Reverse transcriptase (RNA-dependent DNA
35 polymerase)
OCBBF3004487//Platelet-derived growth factor (PDGF)// DEAD/DEAH

box helicase
 OCBBF3005330//Domain found in Dishevelled, Egl-10, and
 Pleckstrin// TCP-1/cpn60 chaperonin family// TCP-1/cpn60
 chaperonin family

5 OCBBF3006986//Beige/BEACH domain// WD domain, G-beta repeat// WD
 domain, G-beta repeat
 OCBBF3008392//DNA binding domain with preference for A/T rich
 regions// PHD-finger// Bromodomain
 OCBBF3008835//Collagen triple helix repeat (20 copies)

10 OCBBF3019269//CXXC zinc finger
 OCBBF3020263//KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type
 OCBBF3021086//Influenza RNA-dependent RNA polymerase subunit
 PA// Reprolysin family propeptide// Leptin
 OCBBF3021361//ELM2 domain// Myb-like DNA-binding domain
 OCBBF3021502//Leptin

20 OCBBF3022827//A20-like zinc finger// Vacuolar sorting protein 9
 (VPS9) domain
 OCBBF3023175//Protein phosphatase 2C// Beige/BEACH domain// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-
 beta repeat// WD domain, G-beta repeat

25 OCBBF3023913//R3H domain// Retroviral Vif (Viral infectivity)
 protein
 OCBBF3025475//Sodium:sulfate symporter transmembrane region//
 Sodium:sulfate symporter transmembrane region
 OCBBF3025503//Vesiculovirus phosphoprotein// haloacid

30 dehalogenase-like hydrolase
 OCBBF3026088//Fatty acid desaturase
 OCBBF3026361//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// RNA polymerases M/15 Kd

subunits

- OCBBF3026979//Laminin G domain// Thrombospondin N-terminal -like domains// von Willebrand factor type C domain// von Willebrand factor type C domain// EGF-like domain// EB module// EGF-like domain// Plant PEC family metallothionein// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// Metallothionein// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// von Willebrand factor type C domain// von Willebrand factor type C domain
- 10 OCBBF3027969//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Myosin head (motor domain)
OCBBF3028001//Transmembrane region cyclic Nucleotide Gated Channel
PEBLM2001803//Vacuolar sorting protein 9 (VPS9) domain
- 15 PEBLM2005615//7 transmembrane receptor (rhodopsin family)// Herpesvirus glycoprotein M
PEBLM2006298//Kinesin motor domain
PLACE5000492//Viral RNA dependent RNA polymerase//
Phosphatidylinositol-specific phospholipase C, X domain//
- 20 Phosphatidylinositol-specific phospholipase C, X domain// C2 domain
PLACE6000055//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
PLACE6001933//Receptor L domain
- 25 PLACE6003004//Signal peptidase I// Mandelate racemase / muconate lactonizing enzyme family
PLACE6010925//Ribosomal protein S11
PLACE6010936//7 transmembrane receptor (rhodopsin family)
PLACE6019600//Ras family
- 30 PLACE7000266//Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain
- 35 PLACE7002303//Homeobox domain
PLACE7003985//Prokaryotic molybdopterin oxidoreductases// short

chain dehydrogenase
 PLACE7004103//KH domain// KH domain// KH domain// KH domain//
 Dynamin central region// Domain of unknown function// KH
 domain// KH domain// KH domain// Small cytokines
 5 (intecrine/chemokine), interleukin-8 like// Fanconi anaemia
 group C protein// KH domain// KH domain// AIR carboxylase// KH
 domain
 PLACE7004961//Dynamin GTPase effector domain
 PLACE7005169//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 PLACE7006090//Glycosyl hydrolases family 31
 PLACE7006498//ADP-ribosylation factor family// G-protein alpha
 15 subunit
 PLACE7007379//Zinc carboxypeptidase
 PLACE7007973//Matrix protein (MA), p15// Matrix protein (MA),
 p15// Gag P30 core shell protein// Zinc finger, CCHC class
 PLACE7008136//Reverse transcriptase (RNA-dependent DNA
 20 polymerase)
 PLACE7009563//Arginase family// MAGE family
 PLACE7009757//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 PLACE7009936//RhoGAP domain
 25 PLACE7011559//Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Integrin alpha cytoplasmic
 region
 PLACE7012111//Reprolysin family propeptide// Reprolysin (M12B)
 family zinc metalloprotease// Keratin, high sulfur B2 protein//
 30 Disintegrin// EGF-like domain
 PLACE7014247//Phosphatidylinositol 3- and 4-kinases
 PLACE7016526//ATP-dependent protease La (LON) domain// NB-ARC
 domain// Adenylylsulfate kinase// IstB-like ATP binding
 protein// Shikimate kinase// Isopentenyl transferase// ATPases
 35 associated with various cellular activities (AAA)
 PLACE7018304//PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2

domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain//
 PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2
 domain
 PLACE7018512//Zinc finger, C2H2 type// Zinc finger, C2H2 type
 5 PROST2002078//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 PUAEN2000594//Poly-adenylate binding protein, unique domain.
 PUAEN2000684//Geminivirus AL2 protein// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 10 Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 PUAEN2006639//WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 WD domain, G-beta repeat// WD domain, G-beta repeat
 15 SKMUS2008585//Dual specificity phosphatase, catalytic domain
 SKMUS2009557//Hydroxyethylthiazole kinase family
 SMINT2010753//TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// PPR repeat// TPR Domain
 SMINT2011406//Dynamin GTPase effector domain
 20 SMINT2011509//DNA polymerase X family
 SMINT2014721//E2 (early) protein, N terminal// Carnitine
 acyltransferase
 SMINT2017964//PH domain
 SPLEN2007689//PX domain// SH3 domain
 25 SPLEN2012571//SCAN domain// KRAB box// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type
 SPLEN2022785//Polyomavirus coat protein
 SPLEN2025012//Immunoglobulin domain// Immunoglobulin domain//
 30 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 SPLEN2028417//Homeobox domain
 SPLEN2036608//Zinc finger C-x8-C-x5-C-x3-H type (and similar).
 STOMA2004663//Immunoglobulin domain
 35 SYNOV2003326//TSC-22/dip/bun family
 SYNOV2017179//Hepatitis C virus non-structural protein NS4a//

TBC domain
 SYNOV4003174//Phosphoribulokinase// Myosin head (motor domain)
 SYNOV4009139//Hyaluronidase
 SYNOV4009575//WD domain, G-beta repeat// Gram-negative pili
 5 assembly chaperone// WD domain, G-beta repeat// WD domain, G-
 beta repeat
 T1ESE2000609//DNA polymerase (viral) C-terminal domain// G-patch
 domain// Double-stranded RNA binding motif
 T1ESE2000904//KRAB box// Zinc finger, C2H2 type// Zinc finger,
 10 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 T1ESE2002665//Amino acid permease
 TBAES2003917//Ank repeat// Ank repeat// Ank repeat// Ank repeat
 TBAES2007428//Scorpion short toxins// EGF-like domain// EGF-like
 20 domain
 TESOP2002005//E7 protein, Early protein
 TESTI2001364//Pyridine nucleotide-disulphide oxidoreductase//
 lactate/malate dehydrogenase
 TESTI2005112//Respiratory-chain NADH dehydrogenase, 30 Kd
 25 subunit
 TESTI2005564//EF hand
 TESTI2006543//Collagen triple helix repeat (20 copies)
 TESTI2007490//UDP-glucuronosyl and UDP-glucosyl transferases
 TESTI2009739//Tropomyosins// Domain of unknown function
 30 TESTI2011020//Keratin, high sulfur B2 protein
 TESTI2018335//NADH-ubiquinone/plastoquinone oxidoreductase chain
 4L// Transmembrane amino acid transporter protein// Amino acid
 permease
 TESTI2018867//FF domain
 35 TESTI2021112//Carbamoyl-phosphate synthase (CPSase)
 TESTI2021654//Glycosyl hydrolases family 11

TESTI2022323//7 transmembrane receptor (rhodopsin family)
 TESTI2023903//Ubiquitin family// Gram-negative pili assembly
 chaperone
 TESTI2024267//Transmembrane amino acid transporter protein// Ion
 5 transport protein
 TESTI2030901//Glutathione S-transferases.
 TESTI2034913//Intermediate filament proteins// Intermediate
 filament proteins
 TESTI2036285//Ubiquitin family// Ubiquitin family// Ubiquitin
 10 family
 TESTI2036822//Integral membrane protein// AN1-like Zinc finger//
 DHHC zinc finger domain
 TESTI2037877//Flavin containing amine oxidase
 TESTI2040377//Phorbol esters/diacylglycerol binding domain (C1
 15 domain)// Zinc finger, C3HC4 type (RING finger)// PHD-finger//
 Zinc finger present in dystrophin, CBP/p300// Zinc finger, C3HC4
 type (RING finger)
 TESTI2049041//TPR Domain// TPR Domain
 TESTI2049062//short chain dehydrogenase
 20 TESTI2052670//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 TESTI4000370//Keratin, high sulfur B2 protein// Bacterial
 regulatory proteins, gntr family
 25 TESTI4000621//SNF2 and others N-terminal domain// 6-O-
 methylguanine DNA methyltransferase// Rel homology domain
 (RHD).// Helicases conserved C-terminal domain
 TESTI4001517//Intermediate filament proteins
 TESTI4001569//Leucine Rich Repeat// Leucine Rich Repeat//
 30 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 Repeat// KE2 family protein// Leucine Rich Repeat// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 35 Repeat// Leucine Rich Repeat
 TESTI4001679//FYVE zinc finger// Zinc finger, C3HC4 type (RING

finger)// PHD-finger
 TESTI4002141//Keratin, high sulfur B2 protein
 TESTI4002774//PH domain// Phosphoglycerate mutase family//
 Oxysterol-binding protein
 5 TESTI4002799//RNA polymerase beta subunit// PHD-finger
 TESTI4002868//Metallothionein
 TESTI4003404//Ank repeat// Ank repeat// Ank repeat// PEP-
 utilizing enzymes
 TESTI4003565//Inositol monophosphatase family
 10 TESTI4003602//Translation initiation factor IF-3// Divalent
 cation transporter
 TESTI4003703//Inositol monophosphatase family
 TESTI4003796//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 TESTI4003944//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Domain of
 unknown function// Zinc finger, C2H2 type// Zinc finger, C2H2
 20 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 TESTI4004031//Domain of unknown function
 25 TESTI4004539//Integral membrane protein// Sodium Bile acid
 symporter family
 TESTI4004695//Leptin
 TESTI4005322//KRAB box// Fungal cellulose binding domain// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 30 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-
 type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type
 TESTI4005399//Divalent cation transporter// Divalent cation
 35 transporter
 TESTI4005470//Zinc finger, C2H2 type// Zinc finger, C2H2 type//

- Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- 5 TESTI4005653//Collagen triple helix repeat (20 copies)
TESTI4007671//Thioredoxin
TESTI4007965//Adaptin N terminal region// Gamma-adaptin, C-terminus
TESTI4008305//Collagen triple helix repeat (20 copies)//
- 10 Herpesvirus Glycoprotein B
TESTI4010544//Cytochrome C and Quinol oxidase polypeptide I// Sodium/hydrogen exchanger family// Ion transport protein// Cyclic nucleotide-binding domain
TESTI4010721//Ribonucleotide reductase
- 15 TESTI4010902//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
TESTI4011926//Gag P30 core shell protein
TESTI4012960//Influenza RNA-dependent RNA polymerase subunit
- 20 PA// Reprolysin family propeptide// Leptin
TESTI4013474//Nuclear transition protein 2// Phorbol esters/diacylglycerol binding domain (C1 domain)// RhoGAP domain
TESTI4013742//Leucine Rich Repeat// Leucine Rich Repeat// Hantavirus nucleocapsid protein// Troponin// Formin Homology 2
- 25 Domain// Apolipoprotein A1/A4/E family
TESTI4014415//Ribosomal protein S8// Uncharacterized protein family// Domain of unknown function// Sodium/hydrogen exchanger family// Ion transport protein// Cyclic nucleotide-binding domain
- 30 TESTI4017854//Hepatitis C virus non-structural protein E2/NS1
TESTI4020342//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Protein phosphatase 2A regulatory subunit PR55// WD domain, G-beta
- 35 repeat
TESTI4020596//Calpain family cysteine protease// Calpain large

subunit, domain III// C2 domain
 TESTI4020819//Clq domain
 TESTI4021129//GAF domain
 TESTI4021197//C2 domain// PDZ domain (Also known as DHR or
 5 GLGF).// Regulator of G protein signaling domain// Regulator of
 G protein signaling domain
 TESTI4021569//ABC transporter transmembrane region.
 TESTI4022158//Immunoglobulin domain// Thrombospondin type 1
 domain// Thrombospondin type 1 domain// ZU5 domain// Death
 10 domain
 TESTI4023096//ABC 3 transport family// Amino acid permease//
 Cystatin domain
 TESTI4024294//Chorion protein
 TESTI4024494//Zinc finger, C3HC4 type (RING finger)//
 15 Peroxidase// Zinc finger, C3HC4 type (RING finger)// B-box zinc
 finger// Scorpion short toxins
 TESTI4026080//Nucleosome assembly protein (NAP)// Lipoate-
 protein ligase B// Asparaginase// ABC transporter
 TESTI4028042//WD domain, G-beta repeat// WD domain, G-beta
 20 repeat// WD domain, G-beta repeat// Fibrillar collagen C-
 terminal domain
 TESTI4028182//3'5'-cyclic nucleotide phosphodiesterase//
 Elongation factor Tu family
 TESTI4029731//Ras family
 25 TESTI4030864//Ribosomal protein L36
 TESTI4031066//Lipoate-protein ligase B// KE2 family protein
 TESTI4031173//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TESTI4032128//Amyloid A4 extracellular domain// Kunitz/Bovine
 30 pancreatic trypsin inhibitor domain
 TESTI4032913//Zinc finger present in dystrophin, CBP/p300// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat
 TESTI4033177//K-box region// Dual specificity phosphatase,
 35 catalytic domain// Penicillin amidase
 TESTI4035898//Kelch motif// Kelch motif// Kelch motif

TESTI4036048//PX domain
 TESTI4037949//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Glycophorin A// Kelch motif// Kelch motif
 TESTI4039451//Adaptin N terminal region
 5 TESTI4039904//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 10 type
 TESTI4040559//Transmembrane region cyclic Nucleotide Gated Channel// Cyclic nucleotide-binding domain
 TESTI4040598//Cytochrome P450
 TESTI4041049//Calponin homology (CH) domain
 15 TESTI4041482//Archaeal ATPase
 TESTI4041984//EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// EB module// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// TB domain// EGF-like domain// EGF-like domain// TB domain// EGF-like domain// EGF-like domain
 20 domain// EGF-like domain
 TESTI4043166//Formin Homology 2 Domain
 TESTI4046073//Dockerin domain type I// RhoGAP domain
 TESTI4046873//TPR Domain// TPR Domain// TPR Domain// TPR Domain
 TESTI4047328//von Willebrand factor type D domain// Trypsin
 25 Inhibitor like cysteine rich domain// Chitin binding domain// von Willebrand factor type D domain// Trypsin Inhibitor like cysteine rich domain// Metallothionein
 TESTI4047569//Keratin, high sulfur B2 protein
 TESTI4047808//Eukaryotic protein kinase domain// Eukaryotic
 30 protein kinase domain
 TESTI4049786//Mur ligase family// Hexokinase// Hexokinase
 TESTI4049899//Scavenger receptor cysteine-rich domain// CUB domain
 TESTI4051015//Major intrinsic protein// Major intrinsic protein
 35 TESTI4051054//B-box zinc finger.
 TESTI4051424//Immunoglobulin domain// Fibronectin type III

domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Aldo/keto reductase family// Immunoglobulin domain//
 Thioredoxin// Immunoglobulin domain// Immunoglobulin domain
 5 TESTI4051865//PDZ domain (Also known as DHR or GLGF).// Collagen
 triple helix repeat (20 copies)// PDZ domain (Also known as DHR
 or GLGF).// PDZ domain (Also known as DHR or GLGF).// SH3
 domain// Ribosomal protein L15 amino terminal region// Guanylate
 kinase
 10 TESTI4052219//E1-E2 ATPase// E1-E2 ATPase// GTP cyclohydrolase
 II
 TESTI4052598//Lectin C-type domain
 TESTI4052775//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger,
 15 C2H2 type
 THYMU2008207//Zinc finger, C3HC4 type (RING finger)
 THYMU2038199//Zinc finger, C2H2 type// Zinc finger, C2H2 type
 THYMU3000390//Ribonuclease T2 family
 THYMU3002825//Flp family// Glycosyl hydrolase family 47
 20 THYMU3003007//TPR Domain
 THYMU3008105//Zinc finger, C2H2 type// FYVE zinc finger// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-
 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 25 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 THYMU3012402//Armadillo/beta-catenin-like repeats//
 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// Armadillo/beta-catenin-like repeats//
 30 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats
 THYMU3012983//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 35 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription

```
factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
finger, C2H2 type
```

THYMU3013785//RasGEF domain

- 5 THYMU3014173//Class I Histocompatibility antigen, domains alpha
1 and 2

THYMU3014372//Integrase Zinc binding domain// Aldo/keto
reductase family// MCM2/3/5 family

THYMU3015042//Polyomavirus coat protein

- 10 THYMU3015571//Chaperonins 10 Kd subunit

THYMU3015647//Domain of unknown function// Latrophilin/CL-1-like
GPS domain// CbiM// 7 transmembrane receptor (Secretin family)

THYMU3016518//Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain

- 15 THYMU3017761//Gag P30 core shell protein

THYMU3019476//Matrix protein (MA), p15

THYMU3020221//Immunoglobulin domain// Fibronectin type II
domain// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain

- 20 THYMU3021404//Sugar (and other) transporter

THYMU3021586//Helix-loop-helix DNA-binding domain

THYMU3021755//HCO3- transporter family

THYMU3022434//Zinc finger, C2H2 type// MOZ/SAS family

THYMU3023400//Transmembrane amino acid transporter protein//

- 25 Large-conductance mechanosensitive channel, MscL// CbiM// DNA
gyrase/topoisomerase IV, subunit A

THYMU3025118//Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain

- 30 THYMU3025642//von Hippel-Lindau disease tumor suppressor protein

THYMU3025683//Heavy-metal-associated domain// Vacuolar sorting
protein 9 (VPS9) domain// chorismate binding enzyme// Ras
association (RalGDS/AF-6) domain

THYMU3026000//KRAB box// Zinc finger, C2H2 type// Zinc finger,

- 35 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription

- factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- THYMU3026306//Flp family// Glycosyl hydrolase family 47
- THYMU3026479//Glutathione S-transferases.
- 5 THYMU3026532//Plexin repeat// Integrins, beta chain
- THYMU3030072//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 10 PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain (4 repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- THYMU3030752//K⁺ channel tetramerisation domain
- 15 THYMU3031878//PAP2 superfamily
- THYMU3032798//Eukaryotic protein kinase domain
- THYMU3033626//NOL1/NOP2/sun family
- THYMU3033649//Immunoreceptor tyrosine-based activation motif
- THYMU3034671//Histone deacetylase family
- 20 THYMU3036953//Trypsin
- THYMU3037617//FYVE zinc finger// AN1-like Zinc finger
- THYMU3037772//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- THYMU3038158//Collagen triple helix repeat (20 copies)//
- 25 Collagen triple helix repeat (20 copies)// Collagen triple helix repeat (20 copies)
- THYMU3040126//Metallothionein
- THYMU3040172//Scavenger receptor cysteine-rich domain// Scavenger receptor cysteine-rich domain// Scavenger receptor
- 30 cysteine-rich domain
- THYMU3040746//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- THYMU3040829//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- 35 THYMU3041428//DEAD/DEAH box helicase// Helicases conserved C-terminal domain

- THYMU3043200//Zinc finger, C2H2 type
 THYMU3044075//BTB/POZ domain// K⁺ channel tetramerisation domain
 THYMU3045704//Prokaryotic transcription elongation factor,
 GreA/GreB
- 5 THYMU3046360//F-box domain.
 THYMU3047115//Site-specific recombinases// E1-E2 ATPase// Na⁺/K⁺
 ATPase C-terminus
 THYMU3047891//ThiF family// short chain dehydrogenase
 TKIDN2003396//Zinc finger, CCHC class
- 10 TKIDN2011051//Keratin, high sulfur B2 protein
 TKIDN2011160//Thrombospondin type 1 domain
 TLIVE2001616//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TLIVE2007736//PDZ domain (Also known as DHR or GLGF).
- 20 TLUNG2000654//bZIP transcription factor// Intermediate filament
 proteins
 TLUNG2001445//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
- 25 TLUNG2001600//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TRACH2022113//dUTPase
 TRACH2024730//Phosphoribosyl-ATP pyrophosphohydrolase// Death
 domain
- 30 TRACH3002752//PHD-finger// Zn-finger in ubiquitin-hydrolases and
 other proteins
 TRACH3002890//Collagen triple helix repeat (20 copies)
 TRACH3003037//Phosphotriesterase family// RhoGEF domain// PH
 domain// Thaumatin family// GATA zinc finger// FYVE zinc
 35 finger// PH domain
 TRACH3003357//Interleukin-6/G-CSF/MGF family// SH3 domain// SH3

domain// SH3 domain// SH3 domain
 TRACH3003458//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 5 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 10 C2H2 type// Zinc finger, C2H2 type
 TRACH3004113//Ribosomal protein L37e// FYVE zinc finger// Alpha-
 2-macroglobulin family// Interleukin 4
 TRACH3004412//Zinc finger, CCHC class// Clusterin
 TRACH3004424//Fungal cellulose binding domain// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 20 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 25 TRACH3004747//Sugar (and other) transporter
 TRACH3005173//PH domain
 TRACH3005274//Trans-activation protein X// Glycosyl transferases
 group 1
 TRACH3005699//SEA domain// SEA domain
 30 TRACH3006379//Intermediate filament proteins
 TRACH3006800//Fungalsin metallopeptidase (M36)// SEA domain//
 SEA domain// SEA domain
 TRACH3007689//Ank repeat// Ank repeat// Ank repeat// TPR
 Domain// TPR Domain// TPR Domain
 35 TRACH3009008//Pyridine nucleotide-disulphide oxidoreductase
 TRACH3009061//Papain family cysteine protease// ABC transporter

TRACH3010079//Mov34/MPN/PAD-1 family
 TRACH3010167//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 TRACH3011082//Immunoglobulin domain
 5 TRACH3011184//Immunoglobulin domain
 TRACH3011313//Aminotransferase class IV
 TRACH3011538//RhoGEF domain// PH domain
 TRACH3012106//FERM domain (Band 4.1 family)
 TRACH3012460//Collagen triple helix repeat (20 copies)
 10 TRACH3012659//Immunoglobulin domain
 TRACH3015346//Uncharacterized protein family UPF0004//
 Uncharacterized protein family UPF0004
 TRACH3015354//Lectin (probable mannose binding)
 TRACH3015951//BTB/POZ domain// Zinc finger, C2H2 type// Zinc
 15 finger, C3HC4 type (RING finger)// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type
 20 TRACH3016455//Calpain family cysteine protease// Calpain large
 subunit, domain III
 TRACH3016805//Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat
 TRACH3017409//RNA dependent RNA polymerase
 25 TRACH3018108//FKBP-type peptidyl-prolyl cis-trans isomerases//
 TPR Domain// TPR Domain
 TRACH3018261//Glycosyl hydrolase family 47
 TRACH3018519//WD domain, G-beta repeat
 TRACH3018524//Fibronectin type III domain// Fibronectin type III
 30 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 domain// Fibronectin type III domain// Fibronectin type III
 35 domain// Fibronectin type III domain// Fibronectin type III
 domain

- TRACH3018606//SAM domain (Sterile alpha motif)
 TRACH3018907//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
- 5 TRACH3019058//Immunoglobulin domain// Immunoglobulin domain
 TRACH3019370//ABC transporter
 TRACH3019621//Glycosyl transferase
 TRACH3019807//Immunoglobulin domain
 TRACH3020605//RhoGEF domain// SH3 domain// SH3 domain
- 10 TRACH3020769//Ezrin/radixin/moesin family// Myosin tail
 TRACH3020930//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TRACH3021023//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
- 15 TRACH3021544//Ubiquitin carboxyl-terminal hydrolases family 2//
 Ubiquitin carboxyl-terminal hydrolase family 2
 TRACH3021778//RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 TRACH3022109//DHHC zinc finger domain
- 20 TRACH3022296//DnaJ domain
 TRACH3022758//EF hand// EF hand
 TRACH3023203//Flavivirus polyprotein propeptide
 TRACH3023373//EF hand// EF hand// Reovirus viral attachment
 protein sigma 1// Peptide hormone
- 25 TRACH3023516//FKBP-type peptidyl-prolyl cis-trans isomerases//
 FKBP-type peptidyl-prolyl cis-trans isomerases// FKBP-type
 peptidyl-prolyl cis-trans isomerases// FKBP-type peptidyl-prolyl
 cis-trans isomerases// EF hand// EF hand
 TRACH3024020//Eukaryotic protein kinase domain
- 30 TRACH3024081//E1-E2 ATPase
 TRACH3024342//Metallo-beta-lactamase superfamily
 TRACH3024512//Chitin synthase// von Willebrand factor type A
 domain
 TRACH3025316//Armadillo/beta-catenin-like repeats//
- 35 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// Armadillo/beta-catenin-like repeats// Beta-

lactamase// Armadillo/beta-catenin-like repeats
 TRACH3026299//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TRACH3026303//Rhodanese-like domain// Integrase Zinc binding
 5 domain// Integrase Zinc binding domain
 TRACH3026650//IPT/TIG domain// IPT/TIG domain// IPT/TIG domain//
 Clq domain// EF hand// EF hand// Growth-Arrest-Specific Protein
 2 Domain// Potyvirus P1 protease
 TRACH3027229//Acyltransferase
 10 TRACH3027701//Thermophilic metalloprotease (M29)
 TRACH3028180//SCAN domain// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TRACH3028441//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 20 TRACH3028837//Calponin homology (CH) domain
 TRACH3028855//R3H domain// Uncharacterized protein family
 UPF0024
 TRACH3029329//Fes/CIP4 homology domain// Hrl repeat motif// ENV
 polyprotein (coat polyprotein)// ATP synthase Alpha chain, C
 25 terminal
 TRACH3029462//Spectrin repeat// Spectrin repeat// Protein of
 unknown function// Spectrin repeat// Bacterial flagellin N-
 terminus// Spectrin repeat// Spectrin repeat// Spectrin repeat//
 Caulimovirus movement protein// Spectrin repeat// Spectrin
 30 repeat// Spectrin repeat// UvrB/uvrC motif// Spectrin repeat//
 Spectrin repeat// Spectrin repeat// KE2 family protein
 TRACH3029670//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TRACH3030176//Beige/BEACH domain// WD domain, G-beta repeat// WD
 35 domain, G-beta repeat
 TRACH3030855//Serpins (serine protease inhibitors)

TRACH3031316//Immunoglobulin domain
 TRACH3031660//Regulatory subunit of type II PKA R-subunit//
 Cyclic nucleotide-binding domain// Cyclic nucleotide-binding
 domain
 5 TRACH3031678//Natural resistance-associated macrophage protein
 TRACH3032150//Calcium channel extracellular region// Pyridoxal-
 dependent decarboxylase conserved domain
 TRACH3032570//PDZ domain (Also known as DHR or GLGF).// PDZ
 domain (Also known as DHR or GLGF).
 10 TRACH3034680//Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 TRACH3036103//Immunoglobulin domain
 TRACH3036750//BTK motif// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// GATA zinc
 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Ribonuclease T2
 family
 TRACH3037505//Immunoglobulin domain// Immunoglobulin domain//
 20 Immunoglobulin domain// Immunoglobulin domain
 TRACH3038399//Eukaryotic protein kinase domain// Eukaryotic
 protein kinase domain
 TSTOM2001571//Eukaryotic protein kinase domain
 TUTER2001433//Immunoglobulin domain// Immunoglobulin domain//
 25 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 UTERU2016669//Helix-hairpin-helix motif.// Helix-hairpin-helix
 motif.
 UTERU2024042//Eukaryotic protein kinase domain
 30 UTERU2037423//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 UTERU3001029//WD domain, G-beta repeat// WD domain, G-beta
 35 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 WD domain, G-beta repeat// WD domain, G-beta repeat

UTERU3001394//EGF-like domain
 UTERU3001946//Fungalysin metallopeptidase (M36)// SEA domain//
 SEA domain
 UTERU3006720//RhoGAP domain
 5 UTERU3009775//PDZ domain (Also known as DHR or GLGF).
 UTERU3010409//Immunoglobulin domain
 UTERU3010604//Indoleamine 2,3-dioxygenase
 UTERU3010919//Eukaryotic protein kinase domain// Regulator of
 chromosome condensation (RCC1)// Regulator of chromosome
 10 condensation (RCC1)// Regulator of chromosome condensation
 (RCC1)
 UTERU3011398//von Willebrand factor type A domain
 UTERU3011558//GTPase of unknown function
 UTERU3011579//Plant PEC family metallothionein
 15 UTERU3011837//Fibronectin type III domain
 UTERU3012293//Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 20 C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type
 UTERU3012414//ADP-ribosylation factor family// G-protein alpha
 25 subunit
 UTERU3015011//LIM domain containing proteins// LIM domain
 containing proteins// LIM domain containing proteins// Phorbol
 esters/diacylglycerol binding domain (C1 domain)// PHD-finger//
 LIM domain containing proteins
 30 UTERU3015299//NADH ubiquinone oxidoreductase, 20 Kd subunit
 UTERU3015647//Immunoglobulin domain
 UTERU3016070//SCAN domain// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type

- UTERU3016273//Integral membrane protein
- UTERU3017441//Armadillo/beta-catenin-like repeats//
 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// D-isomer specific 2-hydroxyacid dehydrogenases//
- 5 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats
- UTERU3017626//Ion transport protein// Transmembrane region
 cyclic Nucleotide Gated Channel
- UTERU3017995//UBX domain
- 10 UTERU3018172//Bacterial regulatory proteins, crp family
- UTERU3018255//Thrombospondin type 1 domain
- UTERU3019708//Viral (Superfamily 1) RNA helicase
- UTERU3020090//DNA polymerase (viral) C-terminal domain
- UTERU3021231//PX domain
- 15 UTERU3021850//Thrombospondin type 1 domain// DnaJ central domain
 (4 repeats)
- UTERU3022168//DNA polymerase family B// C2 domain// C2 domain//
 C2 domain// C2 domain// C2 domain
- UTERU3022588//bZIP transcription factor
- 20 UTERU3023141//Double-stranded RNA binding motif
- Deduced amino acid sequences of following 29 clones were
 also detected to have functional domains with Pfam.
- ADRGL2011190// GAF domain// Transposase, Mutator family// 3'5'-
 cyclic nucleotide phosphodiesterase
- 25 BRACE3002184// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
- 30 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
- BRACE3026993// TSC-22/dip/bun family
- BRACE3046450// PDZ domain (Also known as DHR or GLGF).// PDZ
 domain (Also known as DHR or GLGF).// PDZ domain (Also known as
- 35 DHR or GLGF). 1// PDZ domain (Also known as DHR or GLGF).
- BRAMY3008096// Eukaryotic protein kinase domain

- BRAWH3013197// Receptor family ligand binding region// 7
transmembrane receptor (metabotropic glutamate family)
- BRAWH3028645// Latrophilin/CL-1-like GPS domain// FecCD
transport family// 7 transmembrane receptor (Secretin family)
- 5 BRAWH3046240// 7 transmembrane receptor (rhodopsin family)
- BRCAN2019772// Zinc finger, C4 type (two domains)// Ligand-
binding domain of nuclear hormone receptor
- CTONG2002832// KRAB box// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
carboxypeptidase// Zinc finger, C2H2 type// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
type
- 15 CTONG2003764// Phorbol esters/diacylglycerol binding domain (C1
domain)
- PROST2010326// Latrophilin/CL-1-like GPS domain// Cytochrome C
assembly protein// 7 transmembrane receptor (Secretin family)
- TBAES2004105// Thrombospondin type 1 domain
- 20 TBAES2007379// EGF-like domain// EGF-like domain// Trypsin
Inhibitor like cysteine rich domain// EGF-like domain// EGF-like
domain// Keratin, high sulfur B2 protein// EGF-like domain//
EGF-like domain// Granulins// EGF-like domain// EGF-like
domain// EGF-like domain
- 25 TBAES2007481// Cyclin
- TBAES2008133// PDZ domain (Also known as DHR or GLGF).
- TESTI2043585// 7 transmembrane receptor (rhodopsin family)
- TESTI2046536// Sperm histone P2
- TESTI4002988// KRAB box// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 30 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Zinc finger, C2H2 type// DM DNA binding domain//
Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)//
Zinc finger, C2H2 type// Putative zinc finger in N-recogin//
- 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//

- Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- TESTI4005158// Integrins, beta chain// Notch (DSL) domain// Amiloride-sensitive sodium channel
- 5 TESTI4005500// KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DM DNA binding domain// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)//
- 10 Zinc finger, C2H2 type// Putative zinc finger in N-recogin// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- 15 TESTI4052089// Eukaryotic protein kinase domain THYMU3024602// EGF-like domain// EB module// EGF-like domain// Metallothionein// EGF-like domain// EGF-like domain// Keratin, high sulfur B2 protein// EGF-like domain// Latrophilin/CL-1-like GPS domain// Leishmanolysin//7 transmembrane receptor (Secretin
- 20 family) THYMU3044175// S-adenosyl-L-homocysteine hydrolase THYMU3046350// Sodium:neurotransmitter symporter family// Sulfate transporter family// Sodium:neurotransmitter symporter family// Sodium:neurotransmitter symporter family
- 25 TRACH1000193// Metallothionein family 5// Zinc finger, C4 type (two domains)// Ligand-binding domain of nuclear hormone receptor TRACH3019290// KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type
- 30
- 35 TRACH3021066// Furin-like cysteine rich region// Eukaryotic

protein kinase domain

UTERU2036507// Thrombospondin type 1 domain// NTR/C345C module

EXAMPLE 6

5 Functional categorization based on homology search of the full-length nucleotide sequences and deduced amino acid sequences

10 The functional prediction and categorization of the proteins encoded by the clones were carried out based on the result of homology search of the databases of Swiss-Prot, nr, and RefSeq (see the Homology Search Result Data) for the full-length nucleotide sequences and deduced amino acid sequences.

15 A clone predicted to belong to the category of secretory protein/membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, and connective tissue, suggesting that it is a secretory or membrane protein, or means
20 a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

25 A clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

30 A clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, and SH2 domain, suggesting that the clone encodes a signal transduction-related protein.

35 A clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, and homeobox, suggesting that the clone encodes a transcription-related protein.

A clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation and syndrome, suggesting that the clone encodes a disease-related protein, or means a
 5 clone whose full-length nucleotide sequence has hit data for Swiss-Prot, nr, or RefSeq, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and
 10 disease database.

A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, and E. C. No. (Enzyme commission number), suggesting that the clone
 15 encodes an enzyme and/or metabolism-related protein.

A clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, and
 20 apoptosis, suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

A clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, and microtubules, suggesting that the clone
 25 encodes a cytoskeleton-related protein.

A clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, and polyadenylation, suggesting that the clone encodes a nuclear
 30 protein and/or RNA synthesis-related protein.

A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having
 35 hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein,

protein transport, and signal recognition particle, suggesting that the clone encodes a protein synthesis and/or transport-related protein.

5 A clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, and DNA damage, suggesting that the clone encodes a cellular defense-related protein.

10 A clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, suggesting that the clone encodes a development and/or differentiation-related protein.

15 A clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

A clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

20 In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional categories in this classification, and there is the possibility
25 that other functions are newly assigned to the protein.

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 551 clones.

3NB692004045, ADIPS2000069, ADRGL2010315, ASTRO2015162,
BLADE2001031, BLADE2002744, BLADE2007744, BRACE2003628,
30 BRACE2012528, BRACE2013126, BRACE2017397, BRACE2017580,
BRACE2017992, BRACE2023633, BRACE2030039, BRACE2035191,
BRACE3001403, BRACE3001973, BRACE3002264, BRACE3002756,
BRACE3004767, BRACE3004981, BRACE3007869, BRACE3009392,
BRACE3013874, BRACE3013986, BRACE3014523, BRACE3015898,
35 BRACE3018083, BRACE3021517, BRACE3021805, BRACE3022051,
BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024879,

BRACE3026345, BRACE3026456, BRACE3026802, BRACE3028360,
 BRACE3029021, BRACE3030538, BRACE3031372, BRACE3031579,
 BRACE3031728, BRACE3032385, BRACE3032537, BRACE3032980,
 BRACE3033525, BRACE3034964, BRACE3034993, BRACE3037637,
 5 BRACE3037803, BRACE3038570, BRACE3039358, BRACE3039378,
 BRACE3040644, BRACE3040863, BRACE3042326, BRACE3042409,
 BRACE3042432, BRACE3044090, BRACE3046049, BRACE3046466,
 BRACE3048565, BRACE3050504, BRACE3051144, BRACE3051621,
 BRACE3052486, BRALZ2010842, BRALZ2011337, BRALZ2013690,
 10 BRAMY2015516, BRAMY2021098, BRAMY2025495, BRAMY2037609,
 BRAMY2041507, BRAMY2044686, BRAMY2046537, BRAMY3002886,
 BRAMY3004126, BRAMY3007449, BRAMY3009556, BRAMY3009904,
 BRAMY3010654, BRAMY3010902, BRAMY3015549, BRAMY3016829,
 BRAMY3018248, BRAWH2000256, BRAWH2010364, BRAWH2011812,
 15 BRAWH2011958, BRAWH2012866, BRAWH2014053, BRAWH2016209,
 BRAWH2016305, BRAWH3001053, BRAWH3001783, BRAWH3001833,
 BRAWH3003573, BRAWH3005892, BRAWH3008867, BRAWH3010461,
 BRAWH3010657, BRAWH3011907, BRAWH3012005, BRAWH3012662,
 BRAWH3012779, BRAWH3013049, BRAWH3014609, BRAWH3015175,
 20 BRAWH3016123, BRAWH3017259, BRAWH3018063, BRAWH3018548,
 BRAWH3018969, BRAWH3019529, BRAWH3019820, BRAWH3020200,
 BRAWH3020884, BRAWH3021012, BRAWH3021641, BRAWH3022347,
 BRAWH3023156, BRAWH3023274, BRAWH3023415, BRAWH3023421,
 BRAWH3024186, BRAWH3024242, BRAWH3027574, BRAWH3027880,
 25 BRAWH3028223, BRAWH3028754, BRAWH3029806, BRAWH3030810,
 BRAWH3032298, BRAWH3034114, BRAWH3034134, BRAWH3035914,
 BRAWH3036270, BRAWH3038055, BRAWH3038324, BRAWH3040711,
 BRAWH3040900, BRAWH3042132, BRAWH3042772, BRAWH3042996,
 BRAWH3043498, BRAWH3043623, BRAWH3044151, BRAWH3044676,
 30 BRAWH3046196, BRAWH3047063, BRAWH3048374, BRAWH3048724,
 BRAWH3049068, BRAWH3049544, BRCAN2002662, BRCAN2003269,
 BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2015402,
 BRCAN2018269, BRCAN2019653, BRCAN2019907, BRCAN2020234,
 BRCAN2020412, BRCAN2020972, BRCAN2021325, BRCAN2022126,
 35 BRCOC2006164, BRCOC2006639, BRCOC2009638, BRHIP2006921,
 BRHIP2020930, BRHIP2021929, BRHIP3000859, BRHIP3001878,

BRHIP3002000, BRHIP3002124, BRHIP3003063, BRHIP3003306,
 BRHIP3003395, BRHIP3004774, BRHIP3005801, BRHIP3005944,
 BRHIP3006950, BRHIP3007195, BRHIP3007424, BRHIP3007960,
 BRHIP3008320, BRHIP3010289, BRHIP3011269, BRHIP3011831,
 5 BRHIP3012185, BRHIP3012357, BRHIP3012997, BRHIP3013078,
 BRHIP3016032, BRHIP3017146, BRHIP3017558, BRHIP3019956,
 BRHIP3020733, BRHIP3021019, BRHIP3025795, BRHIP3025844,
 BRHIP3027160, BRHIP3027191, BRHIP3028742, BRHIP3029530,
 BRHIP3030230, BRHIP3031733, BRHIP3035222, BRHIP3035754,
 10 BRHIP3036715, BRHIP3036936, BRHIP3037810, BRHIP3039430,
 BRHIP3039509, BRSSN2004710, BRSSN2018218, BRSTN2010089,
 BRSTN2011688, BRSTN2011899, BRSTN2011961, BRTHA2000969,
 BRTHA2003759, BRTHA2012189, BRTHA2014647, BRTHA2018304,
 BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566,
 15 BRTHA2020721, BRTHA2020781, BRTHA2021212, BRTHA2021440,
 BRTHA2021450, BRTHA2022914, BRTHA2022968, BRTHA2023437,
 BRTHA2026311, BRTHA2027250, BRTHA2030036, BRTHA2031917,
 BRTHA2033155, BRTHA2033320, BRTHA2033469, BRTHA2033683,
 BRTHA2036055, BRTHA2036295, BRTHA3003225, BRTHA3006593,
 20 BRTHA3010135, BRTHA3010540, BRTHA3010717, BRTHA3011194,
 BRTHA3011998, BRTHA3012265, BRTHA3013882, BRTHA3014835,
 BRTHA3016616, BRTHA3018623, BRTHA3026161, BRTHA3027820,
 BRTHA3028505, CHONS2001287, CHONS2001797, CHONS2002419,
 COLON2004351, COLON2005623, COLON2005735, CTONG2008989,
 25 CTONG2020582, CTONG2027150, CTONG3001605, CTONG3002588,
 CTONG3008223, FCBBF3012443, FEBRA2023498, FEBRA2026977,
 FEHRT2002708, FEKID2002231, FEKID2002493, FELNG2000720,
 FELNG2001706, HCHON2009766, HSYRA2004550, JCMLC1000159,
 JCMLC2000273, JCMLC2002095, JCMLC2002751, KIDNE2004531,
 30 KIDNE2015987, KIDNE2017153, LYMPB1000158, LYMPB2002236,
 LYMPB2002458, LYMPB2002478, MESAN2014624, NETRP2004090,
 NETRP2004434, NETRP2005282, NETRP2005849, NETRP2008582,
 NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3009524,
 NT2RP7019682, NT2RP8001605, NT2RP8003787, NT2RP8008057,
 35 OCBBF2000831, OCBBF2004478, OCBBF2007039, OCBBF2009536,
 OCBBF2018229, OCBBF2018618, OCBBF2036019, OCBBF3003745,

OCBBF3007704, OCBBF3021502, OCBBF3022123, OCBBF3022576,
OCBBF3023175, OCBBF3023993, OCBBF3025475, OCBBF3025887,
OCBBF3026979, OCBBF3028001, PEBLM2003935, PEBLM2005615,
PLACE5000522, PLACE6000012, PLACE6010936, PLACE6019674,
5 PLACE7000266, PLACE7000707, PLACE7001759, PLACE7003639,
PLACE7006090, PLACE7006498, PLACE7008136, PLACE7011269,
PLACE7012111, PLACE7016321, PLACE7016454, PUAEN2000684,
SMINT2003641, SPLEN2011252, SPLEN2025012, SPLEN2031004,
SPLEN2034551, SPLEN2035615, SPLEN2042051, STOMA2004663,
10 SYNOV4009139, T1ESE2002665, TBAES2005361, TBAES2007428,
TESOP2008556, TESTI2003768, TESTI2007490, TESTI2018335,
TESTI2022323, TESTI2024267, TESTI2028613, TESTI2036822,
TESTI2037085, TESTI2037657, TESTI2037877, TESTI2046188,
TESTI2049041, TESTI2052670, TESTI4001037, TESTI4002072,
15 TESTI4002889, TESTI4003602, TESTI4004539, TESTI4004653,
TESTI4005399, TESTI4007671, TESTI4010544, TESTI4010721,
TESTI4013774, TESTI4014415, TESTI4014932, TESTI4014977,
TESTI4017647, TESTI4017854, TESTI4019149, TESTI4021197,
TESTI4021377, TESTI4021569, TESTI4022158, TESTI4023096,
20 TESTI4023654, TESTI4024494, TESTI4026680, TESTI4027170,
TESTI4028042, TESTI4031173, TESTI4031818, TESTI4032128,
TESTI4034973, TESTI4035872, TESTI4035989, TESTI4036012,
TESTI4037949, TESTI4038047, TESTI4040559, TESTI4041049,
TESTI4043067, TESTI4043371, TESTI4045168, TESTI4046450,
25 TESTI4047119, TESTI4048296, TESTI4048545, TESTI4051015,
TESTI4051858, TESTI4052219, TESTI4052430, TESTI4052598,
THYMU3002825, THYMU3003007, THYMU3003350, THYMU3008935,
THYMU3009755, THYMU3011360, THYMU3013197, THYMU3014173,
THYMU3015457, THYMU3015647, THYMU3016518, THYMU3018151,
30 THYMU3019605, THYMU3021404, THYMU3022211, THYMU3022528,
THYMU3022668, THYMU3023107, THYMU3023400, THYMU3025118,
THYMU3025313, THYMU3025642, THYMU3026306, THYMU3026532,
THYMU3026869, THYMU3027540, THYMU3028461, THYMU3029795,
THYMU3031878, THYMU3032032, THYMU3033649, THYMU3033754,
35 THYMU3034099, THYMU3034616, THYMU3036310, THYMU3036934,
THYMU3036953, THYMU3037192, THYMU3037772, THYMU3038158,

THYMU3038167, THYMU3040068, THYMU3040126, THYMU3040146,
 THYMU3040172, THYMU3040746, THYMU3040816, THYMU3041918,
 THYMU3042321, THYMU3043688, THYMU3043779, THYMU3044188,
 THYMU3045510, THYMU3047115, THYMU3047156, THYMU3047542,
 5 THYMU3047760, TKIDN2011160, TLIVE2008797, TRACH3003872,
 TRACH3004747, TRACH3005274, TRACH3005699, TRACH3007274,
 TRACH3007625, TRACH3009008, TRACH3009061, TRACH3010382,
 TRACH3011082, TRACH3011184, TRACH3012659, TRACH3012891,
 TRACH3013900, TRACH3014063, TRACH3014580, TRACH3015136,
 10 TRACH3015346, TRACH3016368, TRACH3016885, TRACH3016992,
 TRACH3017409, TRACH3018191, TRACH3018240, TRACH3018524,
 TRACH3018943, TRACH3019058, TRACH3019370, TRACH3019621,
 TRACH3019807, TRACH3020930, TRACH3021023, TRACH3021544,
 TRACH3022758, TRACH3023063, TRACH3023203, TRACH3023516,
 15 TRACH3023945, TRACH3024081, TRACH3024671, TRACH3025346,
 TRACH3026542, TRACH3027681, TRACH3029670, TRACH3031316,
 TRACH3031678, TRACH3032480, TRACH3034680, TRACH3036103,
 TRACH3036278, TSTOM2002682, UTERU3005422, UTERU3010029,
 UTERU3011092, UTERU3011398, UTERU3011837, UTERU3012414,
 20 UTERU3015647, UTERU3016273, UTERU3017626, UTERU3021850,
 UTERU3022168, UTERU3022922, UTERU3023413

The following 19 clones are also predicted to belong to the category of secretory protein and/or membrane protein.

ADRGL2011190, BRACE3046450, BRAWH3013197, BRAWH3028645,
 25 BRAWH3046240, BRTHA3024233, PROST2010326, TBAES2004105,
 TBAES2007379, TBAES2007481, TBAES2008133, TESTI2043585,
 TESTI4005158, THYMU3024602, THYMU3044175, THYMU3046350,
 TLIVE2007192, UTERU2025415, UTERU2036507

The clones predicted to belong to the category of glycoprotein-related protein are the following 114 clones.

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3001403,
 BRACE3001973, BRACE3002264, BRACE3009392, BRACE3026345,
 BRACE3032385, BRACE3039358, BRACE3039378, BRACE3042432,
 BRACE3046466, BRACE3051621, BRAMY3004126, BRAWH2012866,
 35 BRAWH3001783, BRAWH3003573, BRAWH3014609, BRAWH3023156,
 BRAWH3024186, BRAWH3029806, BRAWH3040900, BRAWH3043623,

BRAWH3044151, BRAWH3049544, BRCAN2003269, BRCAN2021325,
 BRHIP3005944, BRHIP3007424, BRHIP3010289, BRHIP3011269,
 BRHIP3011567, BRHIP3030230, BRHIP3036715, BRHIP3036936,
 BRHIP3039509, BRTHA2019726, BRTHA2020721, BRTHA2022968,
 5 BRTHA2025869, BRTHA2027250, BRTHA2031917, BRTHA2033155,
 BRTHA2033683, BRTHA3010135, CHONS2001287, COLON2004351,
 FEKID2002493, FELNG2000720, JCMLC1000159, JCMLC2000273,
 JCMLC2002095, JCMLC2002751, KIDNE2015987, LYMPB2002458,
 NT2RI3005923, NT2RI3009524, OCBBF2000831, OCBBF2004478,
 10 OCBBF2007039, OCBBF2018618, OCBBF3026979, PEBLM2005615,
 PLACE6001933, PLACE6010936, PLACE7006090, PLACE7012111,
 SPLEN2025012, STOMA2004663, T1ESE2002665, TESTI2007490,
 TESTI2022323, TESTI2037657, TESTI2052670, TESTI4001517,
 TESTI4014932, TESTI4031173, THYMU3014173, THYMU3015647,
 15 THYMU3016518, THYMU3020221, THYMU3025118, THYMU3026532,
 THYMU3032032, THYMU3037772, THYMU3040172, TKIDN2011160,
 TLUNG2001445, TRACH3005274, TRACH3009061, TRACH3015136,
 TRACH3018524, TRACH3018907, TRACH3019058, TRACH3019370,
 TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023,
 20 TRACH3023516, TRACH3025346, TRACH3026299, TRACH3028441,
 TRACH3029670, TRACH3031678, TRACH3034680, TRACH3037505,
 TRACH3038399, TUTER2001433, UTERU3011398, UTERU3011837,
 UTERU3015647, UTERU3021850

The following ten clones are also predicted to belong to
 25 the category of glycoprotein-related protein.

BRAWH3013197, BRAWH3046240, PROST2010326, TBAES2004105,
 TESTI2043585, TESTI4005158, THYMU3024602, THYMU3046350,
 TRACH3021066, UTERU2036507

The clones predicted to belong to the category of signal
 30 transduction-related protein are the following 71 clones.

BRACE3002344, BRACE3017253, BRACE3031315, BRACE3036283,
 BRACE3042046, BRACE3044172, BRACE3046491, BRACE3046609,
 BRAMY3009491, BRAMY3015547, BRAMY3017920, BRAWH3017180,
 BRAWH3019026, BRAWH3027806, BRAWH3032340, BRAWH3042438,
 35 BRAWH3047644, BRCAN2010665, BRHIP3006294, BRHIP3011460,
 BRHIP3011567, BRHIP3033557, BRHIP3037543, BRHIP3041587,

BRTHA2026290, BRTHA2035743, BRTHA3011187, BRTHA3021708,
 BRTHA3025073, BRTHA3026916, KIDNE2010049, NIESE2000698,
 OCBBF3005330, OCBBF3006986, OCBBF3009244, OCBBF3025630,
 PLACE6000055, PLACE6001933, PLACE7009936, PLACE7011559,
 5 PLACE7014247, PUAEN2006639, SKMUS2008585, SPLEN2007689,
 TESTI2021654, TESTI2040377, TESTI4010902, TESTI4013474,
 TESTI4046073, TESTI4049786, TESTI4051865, THYMU3013785,
 THYMU3025683, THYMU3032798, TRACH3003037, TRACH3003357,
 TRACH3005173, TRACH3018519, TRACH3018606, TRACH3024020,
 10 TRACH3026650, TRACH3027701, TRACH3029462, TRACH3030176,
 TRACH3038399, TSTOM2001571, TSTOM2002611, UTERU2024042,
 UTERU3001029, UTERU3010919, UTERU3021231

The following four clones are also predicted to belong to the category of signal transduction-related protein.

15 BRHIP3030064, CTONG2003764, PLACE7013963, TRACH3021066

The clones predicted to belong to the category of transcription-related protein are the following 106 clones.

ASTRO2016114, BEAST2000981, BRACE2012947, BRACE2019348,
 BRACE3025719, BRACE3026844, BRACE3034183, BRACE3041162,
 20 BRACE3046152, BRAMY2040915, BRAMY3000692, BRAMY3007078,
 BRAMY3011581, BRAMY3014027, BRAMY3018754, BRAWH3000446,
 BRAWH3005886, BRAWH3011577, BRAWH3013009, BRAWH3013264,
 BRAWH3017477, BRAWH3023172, BRAWH3028796, BRAWH3031342,
 BRAWH3032571, BRAWH3035936, BRAWH3036247, BRAWH3036334,
 25 BRAWH3038827, BRCOC2012386, BRHIP2023735, BRHIP2027077,
 BRHIP2029529, BRHIP3004725, BRHIP3027651, BRHIP3028246,
 BRTHA2024712, BRTHA3000456, BRTHA3003736, BRTHA3010212,
 BRTHA3014000, BRTHA3028339, CHONS2000797, CHONS2002829,
 CTONG2001932, CTONG2011801, D9OST2003106, FCBBF3020030,
 30 FCBBF5000384, HCASM2008154, NETRP2004017, NT2RI3008179,
 NT2RI3009480, NT2RP8003490, NTONG2003805, NTONG2008483,
 OCBBF2016928, OCBBF3005330, OCBBF3008392, OCBBF3020263,
 OCBBF3021361, OCBBF3022166, PLACE7002303, PLACE7005169,
 PLACE7009757, SPLEN2012571, SPLEN2028417, SYNOV2003326,
 35 TIESE2000904, TESTI2040377, TESTI4001679, TESTI4002799,
 TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322,

TESTI4005470, TESTI4039904, TESTI4052775, THYMU3008105,
 THYMU3012983, THYMU3014372, THYMU3020869, THYMU3021586,
 THYMU3022434, THYMU3026000, THYMU3030072, THYMU3037052,
 THYMU3043200, TLIVE2001616, TRACH3003037, TRACH3003458,
 5 TRACH3004424, TRACH3010079, TRACH3010167, TRACH3010342,
 TRACH3015951, TRACH3021883, TRACH3022109, TRACH3028180,
 TRACH3036750, UTERU2037423, UTERU3012293, UTERU3016070,
 UTERU3019708, UTERU3022588

The following seven clones are also predicted to belong to
 10 the category of transcription-related protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI4002988,
 TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of disease-
 related protein are the following 391 clones.

15 ADIPS2000069, ASTRO2015162, ASTRO2016114, ASTRO3000154,
 BLADE2000256, BRACE1000475, BRACE2012838, BRACE2012947,
 BRACE2013009, BRACE2016896, BRACE2017397, BRACE2023744,
 BRACE2027382, BRACE3001403, BRACE3001973, BRACE3002756,
 BRACE3004767, BRACE3009392, BRACE3013418, BRACE3018083,
 20 BRACE3019941, BRACE3020669, BRACE3025719, BRACE3026345,
 BRACE3026802, BRACE3028998, BRACE3036283, BRACE3039378,
 BRACE3040644, BRACE3041059, BRACE3041162, BRACE3042046,
 BRACE3042432, BRACE3043597, BRACE3044172, BRACE3046152,
 BRACE3046466, BRACE3046609, BRACE3051621, BRACE3052321,
 25 BRALZ2010842, BRALZ2013621, BRAMY2041384, BRAMY3000692,
 BRAMY3004126, BRAMY3007078, BRAMY3009491, BRAMY3011501,
 BRAMY3011581, BRAMY3014027, BRAMY3015086, BRAMY3017920,
 BRAMY3018248, BRAWH2002333, BRAWH2012866, BRAWH2014053,
 BRAWH3001638, BRAWH3001783, BRAWH3004335, BRAWH3010602,
 30 BRAWH3011577, BRAWH3011623, BRAWH3017180, BRAWH3017259,
 BRAWH3018548, BRAWH3019026, BRAWH3021580, BRAWH3023156,
 BRAWH3023172, BRAWH3023415, BRAWH3024186, BRAWH3029385,
 BRAWH3029538, BRAWH3031342, BRAWH3032298, BRAWH3032571,
 BRAWH3033513, BRAWH3034668, BRAWH3034775, BRAWH3034890,
 35 BRAWH3036334, BRAWH3038324, BRAWH3038827, BRAWH3040900,
 BRAWH3041492, BRAWH3041556, BRAWH3042438, BRAWH3042447,

BRAWH3042772, BRAWH3043295, BRAWH3043623, BRAWH3044151,
 BRAWH3046424, BRAWH3047565, BRAWH3047644, BRAWH3049544,
 BRCAN2003269, BRCAN2006051, BRCAN2010665, BRCAN2020331,
 BRCAN2021325, BRCOC2012386, BRHIP2008756, BRHIP2023735,
 5 BRHIP2029529, BRHIP3001076, BRHIP3001481, BRHIP3003984,
 BRHIP3004215, BRHIP3004725, BRHIP3005037, BRHIP3005307,
 BRHIP3005673, BRHIP3005801, BRHIP3006449, BRHIP3007609,
 BRHIP3010289, BRHIP3011567, BRHIP3017146, BRHIP3017855,
 BRHIP3021019, BRHIP3023922, BRHIP3025795, BRHIP3027191,
 10 BRHIP3027651, BRHIP3028742, BRHIP3029409, BRHIP3030230,
 BRHIP3032374, BRHIP3035006, BRHIP3036715, BRHIP3037543,
 BRHIP3039509, BRSSN2004710, BRSTN2006466, BRSTN2008475,
 BRSTN2011961, BRSTN2012069, BRSTN2016918, BRTHA2019726,
 BRTHA2020721, BRTHA2020910, BRTHA2024712, BRTHA2025869,
 15 BRTHA2026071, BRTHA2026290, BRTHA2031917, BRTHA2033155,
 BRTHA2033683, BRTHA3003736, BRTHA3010135, BRTHA3010212,
 BRTHA3011187, BRTHA3011998, BRTHA3012265, BRTHA3014547,
 BRTHA3021708, BRTHA3021971, BRTHA3023403, BRTHA3026916,
 BRTHA3027957, CHONS2001287, CHONS2002829, COLON2001829,
 20 COLON2004911, COLON2005735, CTONG2001932, CTONG2010330,
 CTONG2011801, CTONG2014206, D9OST2004417, FCBBF3020030,
 FCBBF3021191, FCBBF3024911, FCBBF5000384, FEBRA2013570,
 FEBRA2026582, FEBRA2028457, FEKID2002637, FELNG2000720,
 FELNG2001953, HCASM2008154, JCMLC1000159, JCMLC2000273,
 25 JCMLC2002095, KIDNE2015987, N1ESE2000698, NETRP2000961,
 NETRP2003448, NETRP2004017, NETRP2008582, NT2RI3008179,
 NT2RI3009480, NT2RI3009524, NT2RP8003787, NT2RP8008057,
 NTONG2003805, OCBBF2004478, OCBBF2007039, OCBBF2018618,
 OCBBF2024589, OCBBF2030927, OCBBF2036019, OCBBF3001202,
 30 OCBBF3004487, OCBBF3008392, OCBBF3020263, OCBBF3022166,
 OCBBF3025475, OCBBF3025503, OCBBF3025630, OCBBF3026979,
 PEBLM2005615, PLACE5000492, PLACE6001933, PLACE6016030,
 PLACE7000266, PLACE7001759, PLACE7002303, PLACE7003985,
 PLACE7004103, PLACE7006090, PLACE7006268, PLACE7006498,
 35 PLACE7007379, PLACE7009563, PLACE7009757, PLACE7009936,
 PLACE7011559, PLACE7012111, PLACE7014247, PLACE7016526,

PUAEN2000594, SKNSH2007306, SMINT2011406, SMINT2011509,
SMINT2014721, SPLEN2007689, SPLEN2012571, SPLEN2025012,
SPLEN2028417, SPLEN2033996, SYNOV2003326, SYNOV4009139,
T1ESE2000609, TESTI2005112, TESTI2007490, TESTI2009739,
5 TESTI2023903, TESTI2030901, TESTI2034913, TESTI2052670,
TESTI4001517, TESTI4001679, TESTI4002868, TESTI4003796,
TESTI4003944, TESTI4004653, TESTI4005322, TESTI4005653,
TESTI4007965, TESTI4017382, TESTI4017647, TESTI4018436,
TESTI4020596, TESTI4021197, TESTI4021569, TESTI4021713,
10 TESTI4023096, TESTI4026080, TESTI4028182, TESTI4031173,
TESTI4032128, TESTI4032834, TESTI4032913, TESTI4033177,
TESTI4036048, TESTI4039575, TESTI4039904, TESTI4041984,
TESTI4046073, TESTI4047119, TESTI4049786, TESTI4049899,
TESTI4051015, TESTI4052775, THYMU3002825, THYMU3008105,
15 THYMU3012402, THYMU3012983, THYMU3013785, THYMU3014173,
THYMU3014372, THYMU3014620, THYMU3016518, THYMU3020221,
THYMU3020869, THYMU3021586, THYMU3021755, THYMU3022434,
THYMU3023400, THYMU3025118, THYMU3026306, THYMU3026532,
THYMU3027671, THYMU3032032, THYMU3032798, THYMU3033649,
20 THYMU3033759, THYMU3037052, THYMU3037772, THYMU3038158,
THYMU3038375, THYMU3040172, THYMU3040746, THYMU3040816,
THYMU3040829, THYMU3043200, THYMU3047115, THYMU3047760,
TKIDN2011160, TLIVE2007736, TLUNG2000654, TLUNG2001445,
TLUNG2001600, TRACH2024730, TRACH3004424, TRACH3005173,
25 TRACH3005191, TRACH3005699, TRACH3006379, TRACH3006800,
TRACH3008042, TRACH3009008, TRACH3009701, TRACH3010079,
TRACH3010167, TRACH3010342, TRACH3011282, TRACH3011313,
TRACH3011503, TRACH3012891, TRACH3015951, TRACH3016455,
TRACH3016805, TRACH3018524, TRACH3018907, TRACH3019058,
30 TRACH3019621, TRACH3020769, TRACH3020930, TRACH3021023,
TRACH3021373, TRACH3021778, TRACH3021883, TRACH3023373,
TRACH3023960, TRACH3024081, TRACH3024671, TRACH3025346,
TRACH3026283, TRACH3026299, TRACH3028441, TRACH3028597,
TRACH3028837, TRACH3029670, TRACH3030855, TRACH3031660,
35 TRACH3031678, TRACH3032570, TRACH3034680, TRACH3036750,
TRACH3037505, TRACH3038399, TUTER2001433, UTERU2024042,

UTERU2037423, UTERU3001946, UTERU3004635, UTERU3011398,
 UTERU3012293, UTERU3012414, UTERU3012999, UTERU3015011,
 UTERU3015299, UTERU3016308, UTERU3017441, UTERU3017626,
 UTERU3019708, UTERU3021850, UTERU3022588

5 The following 23 clones are also predicted to belong to the
 category of disease-related protein.

ADRGL2011190, BRACE3002184, BRACE3026993, BRACE3046450,
 BRAWH3013197, BRAWH3046240, BRCAN2019772, BRHIP3030064,
 BRTHA3024233, CTONG2002832, CTONG2003764, PROST2010326,
 10 TBAES2004105, TESTI2046536, TESTI4005158, TESTI4005500,
 THYMU3024602, THYMU3046350, TRACH1000193, TRACH3019290,
 TRACH3021066, UTERU2017492, UTERU2036507

15 In particular, hit data of the following 390 clones for
 Swiss-Prot, or nr or RefSeq corresponded to genes or proteins
 which had been deposited in the Online Mendelian Inheritance in
 Man (OMIM), which is the human gene and disease database (the
 OMIM Number is shown in the parenthesis after the Clone Name).

ADIPS2000069(146900), ASTRO2015162(606106), ASTRO2016114(603899),
 ASTRO3000154(601594), BLADE2000256(140750), BRACE1000475(600696),
 20 BRACE2012838(605032), BRACE2012947(140580), BRACE2013009(605888),
 BRACE2016896(601421), BRACE2017397(115437), BRACE2023744(600763),
 BRACE2027382(606019), BRACE3001403(126141), BRACE3001973(600976),
 BRACE3002756(603143), BRACE3004767(182790), BRACE3009392(600229),
 BRACE3013418(182900), BRACE3018083(605268),
 25 BRACE3019941(600595), BRACE3020669(603917), BRACE3025719(605493),
 BRACE3026345(147470), BRACE3026802(605784), BRACE3028998(603063),
 BRACE3036283(602052), BRACE3039378(604100), BRACE3040644(603159),
 BRACE3041059(603486), BRACE3041162(194556), BRACE3042046(311030),
 BRACE3042432(192321), BRACE3043597(603704), BRACE3044172(601231),
 30 BRACE3046152(604950), BRACE3046466(604210;600105),
 BRACE3046609(606457), BRACE3051621(601313;173900),
 BRACE3052321(603050),
 BRALZ2010842(212138), BRALZ2013621(600712), BRAMY2041384(114070),
 BRAMY3000692(603971), BRAMY3004126(603071), BRAMY3007078(602410),
 35 BRAMY3009491(600286), BRAMY3011501(602869), BRAMY3011581(601243),
 BRAMY3014027(194542), BRAMY3015086(602879), BRAMY3017920(600365),

BRAMY3018248(605464), BRAWH2002333(171891), BRAWH2012866(185605),
 BRAWH2014053(604581), BRAWH3001638(605003), BRAWH3001783(605514),
 BRAWH3004335(603244), BRAWH3010602(603216),
 BRAWH3011577(601139), BRAWH3011623(164020), BRAWH3017180(601441),
 5 BRAWH3017259(603143), BRAWH3018548(193065), BRAWH3019026(602033),
 BRAWH3021580(179838), BRAWH3023156(137190), BRAWH3023172(603755),
 BRAWH3023415(604346), BRAWH3024186(179590), BRAWH3029385(602378),
 BRAWH3029538(600948), BRAWH3031342(603971), BRAWH3032298(601995),
 BRAWH3032571(603277), BRAWH3033513(604054;261510),
 10 BRAWH3034668(603486), BRAWH3034775(605800), BRAWH3034890(606265),
 BRAWH3036334(603971), BRAWH3038324(604249), BRAWH3038827(600574),
 BRAWH3040900(604265), BRAWH3041492(130500), BRAWH3041556(172460),
 BRAWH3042438(125855), BRAWH3042447(606323), BRAWH3042772(602878),
 BRAWH3043295(179030), BRAWH3043623(600976), BRAWH3044151(605421),
 15 BRAWH3046424(300272), BRAWH3047565(606277), BRAWH3047644(605216),
 BRAWH3049544(602273), BRCAN2003269(171060;602347),
 BRCAN2006051(604581), BRCAN2010665(603583), BRCAN2020331(604851),
 BRCAN2021325(114855), BRCOC2012386(602277), BRHIP2008756(605819),
 BRHIP2023735(601670), BRHIP2029529(189972), BRHIP3001076(604673),
 20 BRHIP3001481(176889), BRHIP3003984(603722;223900),
 BRHIP3004215(603294), BRHIP3004725(602075), BRHIP3005037(603526),
 BRHIP3005307(603197), BRHIP3005673(138385), BRHIP3005801(605704),
 BRHIP3006449(604275), BRHIP3007609(426000), BRHIP3010289(603130),
 BRHIP3011567(114207), BRHIP3017146(602878), BRHIP3017855(606406),
 25 BRHIP3021019(176879), BRHIP3023922(156570;250940),
 BRHIP3025795(603877), BRHIP3027191(601746), BRHIP3027651(604589),
 BRHIP3028742(602076), BRHIP3029409(604156), BRHIP3030230(602367),
 BRHIP3032374(603197), BRHIP3035006(604402), BRHIP3036715(142800),
 BRHIP3037543(602052), BRHIP3039509(601328), BRSSN2004710(600127),
 30 BRSTN2006466(138275), BRSTN2008475(605178), BRSTN2011961(176790),
 BRSTN2012069(130590), BRSTN2016918(137780), BRTHA2019726(147100),
 BRTHA2020721(147100), BRTHA2020910(602661), BRTHA2024712(600747),
 BRTHA2025869(162280), BRTHA2026071(605297), BRTHA2026290(602306),
 BRTHA2031917(118946), BRTHA2033155(601873), BRTHA2033683(111000),
 35 BRTHA3003736(133510;234050), BRTHA3010135(179590),
 BRTHA3010212(603971), BRTHA3011187(605837), BRTHA3011998(603264),

BRTHA3012265(605646), BRTHA3014547(182900), BRTHA3021708(602654),
 BRTHA3021971(605609), BRTHA3023403(600597), BRTHA3026916(601619),
 BRTHA3027957(606078), CHONS2001287(146732), CHONS2002829(602981),
 COLON2001829(604399), COLON2004911(603937;180100),
 5 COLON2005735(111690;111700), CTONG2001932(605683),
 CTONG2010330(606088), CTONG2011801(603971), CTONG2014206(605609),
 D9OST2004417(113703), FCBBF3020030(603406), FCBBF3021191(605119),
 FCBBF5000384(601737), FEBRA2013570(248600), FEBRA2026582(300252),
 FEBRA2028457(164035), FEKID2002637(176875), FELNG2000720(601662),
 10 FELNG2001953(603597),
 HCASM2008154(133450), JCMLC1000159(107470;209950),
 JCMLC2000273(120980), JCMLC2002095(600738), KIDNE2015987(191845),
 N1ESE2000698(604734), NETRP2000961(600417), NETRP2003448(179551),
 NETRP2004017(605344), NETRP2008582(103195), NT2RI3008179(603808),
 15 NT2RI3009480(601804), NT2RI3009524(604210;600105),
 NT2RP8003787(605427), NT2RP8008057(603489), NTONG2003805(601781),
 OCBBF2004478(604265), OCBBF2007039(605009), OCBBF2018618(102775),
 OCBBF2024589(602462),
 OCBBF2030927(603897), OCBBF2036019(601825;256000),
 20 OCBBF3001202(140750), OCBBF3004487(142560), OCBBF3008392(605682),
 OCBBF3020263(604077), OCBBF3022166(600848), OCBBF3025475(604148),
 OCBBF3025503(601653;113650), OCBBF3025630(604141),
 OCBBF3026979(602319), PEBLM2005615(600242), PLACE5000492(602142),
 PLACE6001933(131550), PLACE6016030(605442), PLACE7000266(188840),
 25 PLACE7001759(600338), PLACE7002303(601542;180500;137600;604229),
 PLACE7003985(109684), PLACE7004103(142695),
 PLACE7006090(154360), PLACE7006268(603053), PLACE7006498(604394),
 PLACE7007379(603105), PLACE7009563(300344), PLACE7009757(601804),
 PLACE7009936(600365), PLACE7011559(600831), PLACE7012111(602714),
 30 PLACE7014247(601232), PLACE7016526(605490), PUAEN2000594(604679),
 SKNSH2007306(118990), SMINT2011406(147890), SMINT2011509(606343),
 SMINT2014721(606090), SPLEN2007689(233700), SPLEN2012571(603430),
 SPLEN2025012(146900), SPLEN2028417(142995),
 SPLEN2033996(603853), SYNOV2003326(602960), SYNOV4009139(603551),
 35 T1ESE2000609(182465), TESTI2005112(603846), TESTI2007490(601291),
 TESTI2009739(160745), TESTI2023903(605046), TESTI2030901(600436),

TESTI2034913(148060), TESTI2052670(142461), TESTI4001517(148070),
 TESTI4001679(602850), TESTI4002868(601863;209920),
 TESTI4003796(603132), TESTI4003944(603971), TESTI4004653(606106),
 TESTI4005322(603899), TESTI4005653(182465), TESTI4007965(603533),
 5 TESTI4017382(605689), TESTI4017647(603211), TESTI4018436(601754),
 TESTI4020596(602537), TESTI4021197(602189), TESTI4021569(605464),
 TESTI4021713(604105), TESTI4023096(604878), TESTI4026080(605575),
 TESTI4028182(603892), TESTI4031173(190197), TESTI4032128(104776),
 TESTI4032834(300188), TESTI4032913(106410), TESTI4033177(602038),
 10 TESTI4036048(601272), TESTI4039575(600951), TESTI4039904(603899),
 TESTI4041984(604710), TESTI4046073(300118;309801),
 TESTI4047119(606202), TESTI4049786(142600;235700),
 TESTI4049899(601969), TESTI4051015(602974), TESTI4052775(165250),
 THYMU3002825(604346), THYMU3008105(194548), THYMU3012402(600686),
 15 THYMU3012983(194556), THYMU3013785(604722), THYMU3014173(143010),
 THYMU3014372(116945), THYMU3014620(605657), THYMU3016518(147100),
 THYMU3020221(147100), THYMU3020869(602550), THYMU3021586(184756),
 THYMU3021755(605024), THYMU3022434(601408), THYMU3023400(605180),
 THYMU3025118(155735), THYMU3026306(604346),
 20 THYMU3026532(600065;116920), THYMU3027671(604143),
 THYMU3032032(604463), THYMU3032798(601212), THYMU3033649(186780),
 THYMU3033759(600495), THYMU3037052(300346), THYMU3037772(147100),
 THYMU3038158(603033;603034), THYMU3038375(181590),
 THYMU3040172(186720), THYMU3040746(147110), THYMU3040816(605704),
 25 THYMU3040829(602649), THYMU3043200(605596), THYMU3047115(108730),
 THYMU3047760(604783), TKIDN2011160(605011),
 TLIVE2007736(604990), TLUNG2000654(148059), TLUNG2001445(146900),
 TLUNG2001600(147130), TRACH2024730(605611), TRACH3004424(603971),
 TRACH3005173(151410), TRACH3005191(605333), TRACH3005699(606154),
 30 TRACH3006379(148059), TRACH3006800(606154), TRACH3008042(166945),
 TRACH3009008(601112), TRACH3009701(603330), TRACH3010079(604850),
 TRACH3010167(601804), TRACH3010342(602943), TRACH3011282(601833),
 TRACH3011313(113520), TRACH3011503(602862),
 TRACH3012891(602397), TRACH3015951(604084), TRACH3016455(605286),
 35 TRACH3016805(106410), TRACH3018524(176882), TRACH3018907(146900),
 TRACH3019058(147170), TRACH3019621(191350), TRACH3020769(160776),

TRACH3020930(147100), TRACH3021023(147170), TRACH3021373(606030),
 TRACH3021778(164035), TRACH3021883(603347), TRACH3023373(159350),
 TRACH3023960(603337), TRACH3024081(605867), TRACH3024671(605942),
 TRACH3025346(603377;212140), TRACH3026283(601517),
 5 TRACH3026299(147170), TRACH3028441(147170), TRACH3028597(604310),
 TRACH3028837(602127), TRACH3029670(147170), TRACH3030855(173321),
 TRACH3031660(176912), TRACH3031678(600523), TRACH3032570(602217),
 TRACH3034680(147170), TRACH3036750(604077), TRACH3037505(147170),
 TRACH3038399(604032;226980), TUTER2001433(146900),
 10 UTERU2024042(602214), UTERU2037423(604077), UTERU3001946(606154),
 UTERU3004635(103390), UTERU3011398(120240;158810;254090),
 UTERU3012293(194556),
 UTERU3012414(604394), UTERU3012999(605567), UTERU3015011(602505),
 UTERU3015299(601825;256000), UTERU3016308(602127),
 15 UTERU3017441(604276), UTERU3017626(603788), UTERU3019708(601430),
 UTERU3021850(605009), UTERU3022588(123811)

Additionally, hit data of the following 23 clones for
 Swiss-Prot, or nr or RefSeq corresponded to genes or proteins
 which had been deposited in the Online Mendelian Inheritance in
 20 Man (OMIM), which is the human gene and disease database (the
 OMIM Number is shown in the parenthesis after the Clone Name).

ADRGL2011190 (602658), BRACE3002184 (603899), BRACE3026993
 (601282), BRACE3046450 (603035), BRAWH3013197 (604100),
 BRAWH3046240 (602646), BRCAN2019772 (603849), BRHIP3030064
 25 (605762), BRTHA3024233 (603088), CTONG2002832 (604668),
 CTONG2003764 (176977), PROST2010326 (604110), TBAES2004105
 (605008), TESTI2046536 (182890; 182882), TESTI4005158 (601328),
 TESTI4005500 (602277), THYMU3024602 (600493), THYMU3046350
 (603080), TRACH1000193 (139139), TRACH3019290 (603975),
 30 TRACH3021066 (164870), UTERU2017492 (602917), UTERU2036507
 (605008)

The clones predicted to belong to the category of enzyme
 and/or metabolism-related protein are the following 164 clones.
 ASTRO2008972, BRACE1000475, BRACE2013132, BRACE2016896,
 35 BRACE2035120, BRACE3017253, BRACE3021805, BRACE3028998,
 BRACE3031315, BRACE3036283, BRACE3041059, BRACE3042409,

BRACE3044172, BRACE3046609, BRAMY3009491, BRAMY3011581,
 BRAWH2002333, BRAWH2014053, BRAWH3001638, BRAWH3004335,
 BRAWH3011331, BRAWH3017180, BRAWH3020928, BRAWH3023415,
 BRAWH3023421, BRAWH3024186, BRAWH3024506, BRAWH3029385,
 5 BRAWH3029806, BRAWH3032571, BRAWH3033513, BRAWH3034668,
 BRAWH3037428, BRAWH3037979, BRAWH3041556, BRAWH3042438,
 BRAWH3043295, BRAWH3044151, BRAWH3046424, BRAWH3047692,
 BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402,
 BRCAN2021325, BRHIP3001481, BRHIP3003126, BRHIP3005307,
 10 BRHIP3005673, BRHIP3007195, BRHIP3007223, BRHIP3011082,
 BRHIP3011269, BRHIP3021019, BRHIP3023922, BRHIP3032374,
 BRHIP3035006, BRHIP3037543, BRHIP3041587, BRSSN2004710,
 BRSTN2006466, BRSTN2011961, BRTHA2005448, BRTHA2010672,
 BRTHA2025869, BRTHA2026311, BRTHA2033155, BRTHA2035743,
 15 BRTHA3003736, BRTHA3010135, BRTHA3010469, BRTHA3023403,
 CHONS2002829, COLON2004351, CTONG2010330, CTONG2020582,
 CTONG3001605, FCBBF3001018, FCBBF3021191, FCBBF5000384,
 FEBRA2013570, FEBRA2026582, FEKID2002637, HSYRA2004550,
 KIDNE2010049, NETRP2000961, NT2RI2004818, NT2RP7016508,
 20 OCBBF2007039, OCBBF2024589, OCBBF2036019, OCBBF3004487,
 OCBBF3005330, OCBBF3009244, PLACE5000492, PLACE6001933,
 PLACE7001759, PLACE7003985, PLACE7004103, PLACE7004961,
 PLACE7006090, PLACE7006268, PLACE7007379, PLACE7011559,
 PLACE7012111, PLACE7014247, PLACE7016526, SKMUS2008585,
 25 SMINT2011509, SMINT2012179, SMINT2014721, SPLEN2007689,
 SYNOV4009139, TBAES2007428, TESTI2005112, TESTI2007490,
 TESTI2021654, TESTI2040377, TESTI2049062, TESTI4000621,
 TESTI4002799, TESTI4007671, TESTI4020596, TESTI4033177,
 TESTI4049786, TESTI4052219, THYMU3002825, THYMU3026306,
 30 THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428,
 THYMU3047115, THYMU3047891, TKIDN2011160, TRACH3005173,
 TRACH3005274, TRACH3009008, TRACH3011313, TRACH3011503,
 TRACH3012891, TRACH3015136, TRACH3016455, TRACH3018108,
 TRACH3018261, TRACH3018524, TRACH3019621, TRACH3021544,
 35 TRACH3022758, TRACH3023516, TRACH3024020, TRACH3024081,
 TRACH3027229, TRACH3027701, TRACH3032150, TRACH3038399,

TSTOM2001571, TSTOM2002611, UTERU2024042, UTERU3010604,
UTERU3010919, UTERU3015299, UTERU3019708, UTERU3021850

The following eight clones are also predicted to belong to the category of enzyme and/or metabolism-related protein.

5 ADRGL2011190, BRHIP3030064, CTONG2003764, PLACE7013963,
TBAES2004105, THYMU3044175, TRACH3021066, UTERU2036507

The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 27 clones.

10 BLADE2000256, BRACE2002392, BRACE3030538, BRACE3036283,
BRACE3044495, BRAMY3002886, BRAMY3009556, BRAWH2016209,
BRAWH3004350, BRAWH3027574, BRCAN2019907, BRHIP3001076,
BRHIP3029409, BRSTN2008475, BRTHA3011265, FEKID2002637,
NT2RP8005546, OCBBF3001202, PLACE7011559, SPLEN2033996,
15 TESTI2023903, TESTI4020819, TESTI4049899, THYMU3014372,
THYMU3021586, UTERU3010919, UTERU3012999

The following two clones are also predicted to belong to the category of cell division and/or cell proliferation-related protein.

20 TBAES2007481, TESTI2046536

The clones predicted to belong to the category of cytoskeleton-related protein are the following 60 clones.

BRACE3004767, BRACE3013418, BRACE3051819, BRAMY3005184,
BRAMY3015086, BRAMY4000915, BRAMY4001652, BRAWH3001783,
25 BRAWH3015175, BRAWH3018548, BRAWH3019026, BRAWH3021580,
BRAWH3021724, BRAWH3027440, BRAWH3027806, BRAWH3029385,
BRAWH3040900, BRAWH3041492, BRCAN2020467, BRHIP3003063,
BRHIP3003340, BRSTN2016918, BRTHA2020910, BRTHA2025869,
BRTHA3014547, BRTHA3025073, CERVX2000968, JCMLC2000273,
30 N1ESE2000698, NT2RI3005923, OCBBF2003518, OCBBF2004478,
OCBBF3027969, PLACE7000266, PLACE7004961, SMINT2010753,
SPLEN2034934, SYNOV4003174, TESTI2001915, TESTI2009739,
TESTI2034913, TESTI4001517, TESTI4004917, TESTI4010902,
TESTI4032913, TESTI4051424, THYMU3026532, TLUNG2000654,
35 TRACH3006379, TRACH3016805, TRACH3020769, TRACH3022960,

TRACH3026650, TRACH3028837, TRACH3029462, TRACH3032570,
UTERU3000670, UTERU3001029, UTERU3015011, UTERU3016308

The following one clone is also predicted to belong to the category of cytoskeleton-related protein.

5 BRACE3026993

The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 40 clones.

10 ASTRO3000154, BRACE3014714, BRACE3036283, BRALZ2013621,
BRAMY3009556, BRAMY3011501, BRAWH3011623, BRAWH3017180,
BRAWH3022651, BRAWH3038252, BRAWH3040695, BRAWH3046424,
BRHIP3004215, BRHIP3007223, BRHIP3020046, BRTHA3010530,
CTONG2006235, FEBRA2028457, NT2RP7016508, OCBBF3001333,
OCBBF3004487, PLACE7004103, PLACE7006268, TESTI2036285,
15 TESTI2037657, TESTI4014932, TESTI4028182, TESTI4032128,
TESTI4033177, TESTI4039575, THYMU3012402, THYMU3040829,
THYMU3041428, TRACH3002752, TRACH3018108, TRACH3021778,
UTERU3004635, UTERU3010409, UTERU3010919, UTERU3013302

20 The following one clone is also predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein.
TESTI2046536

The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 50 clones.

25 BRACE2016896, BRACE2023744, BRACE3020669, BRACE3030538,
BRACE3041059, BRACE3043597, BRAWH2014053, BRAWH3001638,
BRAWH3010602, BRAWH3024506, BRAWH3026349, BRAWH3034668,
BRAWH3037979, BRAWH3041556, BRAWH3044151, BRAWH3047692,
BRCAN2000923, BRCAN2002892, BRCAN2006051, BRCAN2021325,
30 BRHIP3007223, BRSTN2012069, BRTHA2005448, BRTHA2010672,
CHONS2002829, CTONG3001605, D9OST2004417, OCBBF2000831,
OCBBF2007039, PLACE6019600, PLACE7007379, PLACE7012111,
PLACE7016526, TESTI4018436, TESTI4020596, TESTI4032128,
TESTI4036048, THYMU3012402, THYMU3033759, THYMU3036953,
35 THYMU3046360, TKIDN2011160, TRACH3016455, TRACH3018519,

TRACH3021544, TRACH3025316, TRACH3030855, TRACH3038399,
UTERU3014647, UTERU3021850

The following two clones are also predicted to belong to
the category of protein synthesis and/or transport-related
protein.

TBAES2004105, UTERU2036507

The clones predicted to belong to the category of cellular
defense-related protein are the following five clones.

BRACE2012947, BRHIP2029529, BRTHA3003736, THYMU3015571,

TRACH3022296

The clones predicted to belong to the category of
development and/or differentiation-related protein are the
following 16 clones.

ASTRO3000154, BRACE3034964, BRAWH3004350, BRAWH3029538,

BRAWH3038252, BRHIP3007424, BRTHA2024712, BRTHA3011265,

FEKID2002493, NT2RP8003490, NT2RP8006452, OCBBF3025503,

PLACE7002303, TESTI2026024, TRACH3028180, UTERU3016070

The following one clone is also predicted to belong to the
category of development and/or differentiation-related protein.

BRCAN2019772

The clones predicted to belong to the category of DNA-
binding and/or RNA-binding protein are the following 119 clones.

ASTRO2016114, BEAST2000981, BRACE2012947, BRACE2019348,

BRACE3020669, BRACE3025719, BRACE3026844, BRACE3031743,

BRACE3034183, BRACE3041162, BRACE3046152, BRALZ2013621,

BRAMY2040915, BRAMY2046537, BRAMY3000692, BRAMY3007078,

BRAMY3011501, BRAMY3011581, BRAMY3014027, BRAMY3018754,

BRAMY4000962, BRAWH3000446, BRAWH3011577, BRAWH3011623,

BRAWH3013009, BRAWH3013264, BRAWH3017477, BRAWH3028796,

BRAWH3031342, BRAWH3032571, BRAWH3034775, BRAWH3035936,

BRAWH3036247, BRAWH3036334, BRAWH3038827, BRCAN2020331,

BRCOC2012386, BRHIP2027077, BRHIP3004725, BRHIP3028246,

BRSSN2015497, BRTHA2024712, BRTHA3000456, BRTHA3003736,

BRTHA3010212, BRTHA3014000, BRTHA3028339, CHONS2000797,

CHONS2002829, CTONG2001932, CTONG2011801, D9OST2003106,

FCBBF3020030, FCBBF5000384, FEBRA2028457, HCASM2008154,

NETRP2004017, NT2RI3008179, NT2RI3009480, NT2RP7016508,
 NT2RP8003490, NTONG2003805, NTONG2008483, OCBBF2016928,
 OCBBF3004487, OCBBF3008392, OCBBF3020263, OCBBF3021361,
 OCBBF3022166, PLACE7002303, PLACE7004103, PLACE7005169,
 5 PLACE7009757, PROST2002078, PUAEN2000594, SMINT2011509,
 SPLEN2012571, SPLEN2028417, T1ESE2000609, T1ESE2000904,
 TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322,
 TESTI4005470, TESTI4005653, TESTI4032128, TESTI4039575,
 TESTI4039904, TESTI4052775, THYMU3008105, THYMU3012983,
 10 THYMU3014372, THYMU3020869, THYMU3021586, THYMU3026000,
 THYMU3030072, THYMU3033759, THYMU3037052, THYMU3040829,
 TLIVE2001616, TRACH3003458, TRACH3004424, TRACH3005191,
 TRACH3008508, TRACH3010079, TRACH3010167, TRACH3010342,
 TRACH3015951, TRACH3021778, TRACH3021883, TRACH3022109,
 15 TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293,
 UTERU3013302, UTERU3016070, UTERU3022588

The following eight clones are also predicted to belong to the category of DNA-binding and/or RNA-binding protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI2046536,
 20 TESTI4002988, TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 68 clones.

BRACE2013009, BRACE2016896, BRACE3002344, BRACE3014714,
 BRACE3017253, BRACE3036283, BRACE3051819, BRAMY3011501,
 25 BRAMY3018248, BRAWH2014053, BRAWH3015175, BRAWH3024506,
 BRAWH3029385, BRAWH3032571, BRAWH3037428, BRAWH3041556,
 BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2003269,
 BRCAN2006051, BRHIP3007195, BRHIP3027191, BRHIP3041587,
 BRSTN2012069, BRTHA2020910, BRTHA3003736, HSYRA2004550,
 30 KIDNE2010049, NETRP2003448, NT2RP7016508, OCBBF2003518,
 OCBBF3004487, PLACE6001933, PLACE6019600, PLACE7004961,
 PLACE7006498, PLACE7011559, PLACE7016526, PUAEN2006639,
 SMINT2011406, TESTI2009739, TESTI2040377, TESTI4004917,
 TESTI4013474, TESTI4021569, TESTI4028182, TESTI4049786,
 35 TESTI4052219, THYMU3014372, THYMU3032798, THYMU3041428,
 THYMU3047115, TRACH3005191, TRACH3009061, TRACH3009701,

TRACH3012891, TRACH3019370, TRACH3020769, TRACH3022960,
 TRACH3023960, TRACH3024081, TRACH3038399, TSTOM2001571,
 UTERU2024042, UTERU3010919, UTERU3012414, UTERU3019708

The following two clones are also predicted to belong to
 5 the category of ATP binding and/or GTP-binding protein.
 CTONG2003764, TRACH3021066

The 104 clones shown below are clones which were
 unassignable to any of the above-mentioned categories, but have
 been predicted to have some functions based on homology search
 10 using their full-length nucleotide sequences. Clone Name and
 Definition in the result of homology search, demarcated by a
 double slash mark (//), are shown below.

BLADE2002310//SH3-domain binding protein 1 [Homo sapiens]
 BLADE2007799//Hepatocellular carcinoma-associated antigen 66.
 15 BRACE2017359//Mus musculus suppressor of Ty 6 homolog (S.
 cerevisiae) (Supt6h)
 BRACE2017872//nuclear receptor-binding SET-domain protein 1 [Mus
 musculus]
 BRACE3009416//testis specific ankyrin-like protein 1 [Homo
 20 sapiens]
 BRACE3016020//SBBI31 protein [Homo sapiens]
 BRACE3019570//SNAP-25-interacting protein [Rattus norvegicus]
 BRACE3022303//Pax transcription activation domain interacting
 protein [Mus musculus]
 25 BRACE3022340//SNAP-25-interacting protein [Rattus norvegicus]
 BRACE3026290//Homo sapiens lethal giant larvae homolog 2 [Homo
 sapiens]
 BRACE3032631//F-box protein FBX13 [Mus musculus].
 BRACE3040239//Deltex3 [Mus musculus]
 30 BRACE3047482//tripartite motif-containing 9 [Homo sapiens]
 BRACE3049714//NYD-TSPG protein [Homo sapiens]
 BRACE3052410//IDN3 protein [Homo sapiens]
 BRACE3052595//Nim2 [Rattus norvegicus]
 BRALZ2014054//cenexin 2 [Rattus norvegicus].
 35 BRAMY3007471//gene trap locus F3b; transcript expressed during
 hematopoiesis 2 [Mus musculus]

- BRAMY3010321//MRIP-1 protein [Homo sapiens]
 BRAMY3014613//SH3-domain binding protein 1 [Homo sapiens]
 BRAMY4001863//Mus musculus enabled homolog (Drosophila) (Enah), mRNA
- 5 BRAWH2011796//S-100 protein, alpha chain.
 BRAWH3008167//CUB and Sushi multiple domains 1 [Homo sapiens]
 BRAWH3009961//Nim2 [Rattus norvegicus]
 BRAWH3010726//phosphatidylinositol transfer protein, membrane-associated; Drosophila retinal degeneration B [Homo sapiens]
- 10 BRAWH3015017//axonemal dynein light chain p33.
 BRAWH3024231//Tetratricopeptide repeat protein 4.
 BRAWH3026938//semaF cytoplasmic domain associated protein 3; semaphorin cytoplasmic domain-associated protein 3A [Mus musculus]
- 15 BRAWH3027533//rap2 interacting protein x [Homo sapiens].
 BRAWH3030910//Sec23-interacting protein p125 [Homo sapiens]
 BRAWH3031710//serologically defined colon cancer antigen 33 [Homo sapiens]
 BRAWH3033293//synaptopodin [Homo sapiens]
- 20 BRAWH3042568//ventral anterior homeobox containing gene 1 [Mus musculus]
 BRAWH3043034//Mus musculus neuregulin 1 (Nrg1)
 BRAWH3044122//Munc13-1 [Rattus norvegicus]
 BRHIP2026346//lymphocyte specific formin related protein;
- 25 formin-related gene in leukocytes [Mus musculus]
 BRHIP2027563//host cell factor homolog [Homo sapiens]
 BRHIP3002114//rTS beta protein [Homo sapiens]
 BRHIP3003795//cytochrome P450 retinoid metabolizing protein [Homo sapiens]
- 30 BRHIP3006786//peptidylprolyl isomerase (cyclophilin)-like 2; cyclophilin-like protein CyP-60 [Homo sapiens]
 BRHIP3017109//Socs-5 [Mus musculus]
 BRHIP3019643//Homo sapiens gamma tubulin ring complex protein (76p gene) (76P), mRNA
- 35 BRHIP3032148//brain-enriched guanylate kinase-associated [Rattus norvegicus]

- BRSTN2006638//synaptotagmin interacting protein 1 [Rattus norvegicus]
- BRSTN2016892//BUP protein [Homo sapiens]
- BRSTN2016992//DRR1 protein (TU3A protein).
- 5 BRSTN2017151//COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis); COP9 complex S7a [Mus musculus]
- BRTHA2020642//DRR1 protein (TU3A protein).
- BRTHA3018409//synaptotagmin-like 4; granuphilin-a; granuphilin-b; granuphilin
- 10 BRTHA3019183//Ca²⁺-dependent activator protein for secretion; Ca²⁺-dependent activator protein for secretion [Mus musculus]
- CHONS2001834//tumor endothelial marker 7 precursor [Homo sapiens]
- CTONG2009570//rab11 binding protein [Bos taurus].
- 15 CTONG2012123//Mus musculus enabled homolog (Drosophila) (Enah), mRNA
- CTONG2027591//Mus musculus pecanex homolog (Drosophila) (Pcnx), mRNA.
- CTONG3003669//high-glucose-regulated protein 8 [Homo sapiens]
- 20 ERLTF2002178//Kelch-like protein X.
- HHDP2008185//jerky [Mus musculus]
- NT2RI3001573//F-box protein FBL10 [Mus musculus].
- NT2RI3007095//Mus musculus neuregulin 1 (Nrg1), mRNA.
- NT2RP8001363//signal peptide, CUB domain, EGF-like 1 [Mus
- 25 musculus]
- NT2RP8001584//alpha integrin binding protein 63 [Homo sapiens]
- NT2RP8001604//CUB and Sushi multiple domains 1 [Homo sapiens]
- OCBBF3019269//Homo sapiens Dvl-binding protein IDAX (inhibition of the Dvl and Axin complex) (IDAX)
- 30 OCBBF3022827//putative Rab5 GDP/GTP exchange factor homologue [Homo sapiens]
- OCBBF3023913//Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1C (Ppp1r1c)
- PLACE6003004//rTS beta protein [Homo sapiens]
- 35 PLACE6008315//similar to ALPHA-ACTININ, SARCOMERIC (F-ACTIN CROSS LINKING PROTEIN) (D. melanogaster) [Homo sapiens].

- PLACE6010925//NY-REN-50 antigen [Homo sapiens]
 PLACE7012127//AAA-ATPase TOB3 [Homo sapiens]
 PROST2016566//erythroblast macrophage protein [Mus musculus]
 SYNOV2017179//EBP50-PDZ interactor of 64 kD [Homo sapiens]
 5 SYNOV3000345//upregulated by 1,25-dihydroxyvitamin D-3 [Homo sapiens]
 TBAES2003917//NG28 protein [Mus musculus]
 TESTI2001364//lactate dehydrogenase A -like [Homo sapiens]
 TESTI2004601//NYD-TSPG protein [Homo sapiens]
 10 TESTI2009497//GPI-anchored protein p137 (p137GPI).
 TESTI4002774//oxysterol binding protein 2 [Mus musculus]
 TESTI4003579//FH1/FH2 domains-containing protein (Formin homolog overexpressed in spleen) (FHOS).
 TESTI4003703//retinoblastoma-associated protein RAP140 [Homo sapiens]
 15 TESTI4013742//antigen identified by monoclonal antibody 2A8 [Mus musculus]
 TESTI4014908//dedicator of cyto-kinesis 2 [Mus musculus]
 TESTI4018506//tomosyn [Rattus norvegicus]
 20 TESTI4020342//H326 [Homo sapiens]
 TESTI4024294//WW domain binding protein 2 [Mus musculus]
 TESTI4039451//B29 protein [Homo sapiens]
 TESTI4041482//Rattus norvegicus SEC15 homolog (S. cerevisiae) (Sec15), mRNA
 25 TESTI4043166//lymphocyte specific formin related protein; formin-related gene in leukocytes [Mus musculus]
 TESTI4047328//otogelin [Mus musculus]
 THYMU3011717//exocyst component protein 70 kDa homolog (S. cerevisiae)
 30 THYMU3016822//erythroblast macrophage protein [Mus musculus]
 THYMU3026479//secretory pathway component Sec31B-1 [Homo sapiens]
 THYMU3028702//chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated
 35 protein 1; KIAA0159 gene product [Homo sapiens]
 THYMU3029719//AAA-ATPase TOB3 [Homo sapiens]

- THYMU3038347//tumor stroma and activated macrophage protein DLM-1 [Homo sapiens]
 THYMU3038603//WW domain binding protein 2 [Mus musculus]
 THYMU3040830//AD-012 protein [Homo sapiens]
 5 THYMU3041603//gamma-tubulin complex protein 2 [Homo sapiens]
 TKIDN2003396//Homo sapiens paternally expressed 10 (PEG10), mRNA
 TRACH2011057//D-type cyclin-interacting protein 1; MAID protein [Homo sapiens]
 TRACH3004412//clusterin-like 1 (retinal); unknown prepropeptide
 10 specific to rod photoreceptor [Homo sapiens]
 TRACH3012106//erythrocyte protein band 4.1-like 3 [Mus musculus]
 UTERU3009775//PAPIN [Rattus norvegicus]
 UTERU3010892//adaptor-related protein complex 3, delta 1 subunit; adaptin, delta [Homo sapiens]
 15 UTERU3017995//p47 [Homo sapiens]

So far no information suggesting the function of the remaining 879 clones has been provided by the homology search. The functions of these clones may be clarified when an updated database becomes available in future. Clone names are shown
 20 below.

- ADRGL2010594, AHMSC1000138, BLADE2004849, BLADE2006043,
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 UTERU3014906, UTERU3015844, UTERU3016274, UTERU3018172,
 UTERU3018255, UTERU3020090, UTERU3023141

25 Likewise, so far no information suggesting the function of
 six clones shown below has been provided by the homology search.
 The functions of these clones may be clarified when an updated
 database becomes available in future. Clone names are shown
 below.

30 BRAMY3008096, BRAMY3016953, BRHIP3038037, BRTHA3004432,
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EXAMPLE 7

Functional categorization based on a functional domain search
 35 for deduced amino acid sequences

Domains and motifs are minimal functional structures of polypeptides. The structure of a polypeptide is constituted by a collection of such minimal structures, and thus the overall function of a polypeptide is ensured by the resulting structure. Thus, the overall function of a polypeptide can be predicted relatively accurately using data obtained by analysis of domain and motif structures. Furthermore, classifying these results into functional categories in a database allows clones comprising specific functions to be easily selected. Thus, such databases are highly useful in the functional analysis of each clone.

Pfam was used to undertake a domain search for the amino acid sequences deduced from the full-length nucleotide sequences (see Example 5). Based on these results, the proteins encoded by clones 664 and 29 were categorized and their functions predicted. This was performed by referring to domain and motif names, accession numbers for hit data, and detailed descriptions in Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) as well as functional categorizations in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>).

A clone predicted to belong to the category of secretory and/or membrane protein means a clone having domains and motifs, for example, seven-transmembrane receptor, pancreatic hormone peptides, ion transport protein, or fibroblast growth factor, which suggest receptor, ion channel, hormone, or growth factor.

A clone predicted to belong to the category of glycoprotein-related protein means a clone having domains and motifs, for example, immunoglobulin domain or glycosyl transferases group 1, which suggest involvement in glycobiology, such as glycoprotein or glycosyltransferase.

A clone predicted to belong to the category of signal transduction-related protein means a clone having domains and motifs, for example, eukaryotic protein kinase domain, protein phosphatase 2C, or Ras family, which suggest protein kinase, dephosphoenzyme, SH2 domain, or small G protein.

A clone predicted to belong to the category of transcription-related protein means a clone having domains and motifs, for example, bZIP transcription factor, Zinc finger, or C2H2 type, which suggest transcription factor or transcription-controlling protein.

A clone predicted to belong to the category of disease-related protein means a clone having domains and motifs, for example, Wilm's tumor protein or von Hippel-Lindau disease tumor suppressor protein, which suggest proteins with disease-specific expression or that promote or suppress expression, depending on the disease.

A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having domains and motifs, for example, aldehyde dehydrogenase family, chitin synthase, or glucose-6-phosphate dehydrogenase, which suggest transferase, synthase, or hydrolase.

A clone predicted to belong to the category of cell division- and/or cell proliferation-related protein means a clone having domains and motifs, for example, cyclin or cell division protein, which suggest cyclin or cell proliferation-controlling protein.

A clone predicted to belong to the category of cytoskeleton-related protein means a clone having domains and motifs, for example, actin, fibronectin type I domain, or kinesin motor domain, which suggest actin, kinesin, or fibronectin.

A clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having domains and motifs, for example, hepatitis C virus RNA dependent RNA polymerase or DEAD/DEAH box helicase, which suggest splicing factor, RNA synthase, or helicase.

A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having domains and motifs, for example, translation initiation factor SUI1, ubiquitin family, or ribosomal protein L16, which suggest

translation-related protein, ubiquitin-related protein, or ribosomal protein.

A clone predicted to belong to the category of cellular defense-related protein means a clone having domains and motifs, for example, HSP90 protein or DNA mismatch repair protein, which suggest chaperonin or DNA repair protein.

A clone predicted to belong to the category of development- and/or differentiation-related proteins means a clone having domains and motifs, for example, floricaula / leafy protein, which suggest organogenesis-related protein.

A clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having domains and motifs, for example, transcription factor WhiB, B-box zinc finger, or tRNA synthetases class I (C), which suggest DNA/RNA-relating enzyme group including transcription factor and DNA ligase or Zinc-finger related protein.

A clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having domains and motifs, for example, E1-E2 ATPase or Ras family, which suggest ATP/GTP-related enzyme group including ATPase or G protein.

During this functional categorization, if a clone met every criterion of multiple categories as described above, it was grouped into multiple categories. However, the function of a polypeptide is not limited to these functional categories.

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 92 clones.

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 PEBLM2005615, PLACE6010936, PLACE7004103, PLACE7011559,
 5 PLACE7018304, TESTI2018335, TESTI2022323, TESTI2024267,
 TESTI2036822, TESTI4003602, TESTI4004539, TESTI4005399,
 TESTI4008305, TESTI4010544, TESTI4014415, TESTI4021569,
 TESTI4023096, TESTI4026080, TESTI4040559, TESTI4049899,
 THYMU3015647, THYMU3021404, THYMU3023400, THYMU3026532,
 10 THYMU3030752, THYMU3040172, THYMU3044075, TRACH3003357,
 TRACH3004113, TRACH3004747, TRACH3005699, TRACH3006800,
 TRACH3009061, TRACH3019370, TRACH3023373, TRACH3031678,
 TRACH3032150, UTERU3001946, UTERU3016273, UTERU3017626

The following ten clones are also predicted to belong to
 15 the category of secretory protein and/or membrane protein.

BRAWH3013197, BRAWH3028645, BRAWH3046240, BRCAN2019772,
 PROST2010326, TESTI2043585, TESTI4005158, THYMU3024602,
 THYMU3046350, TRACH1000193

The clones predicted to belong to the category of
 20 glycoprotein-related protein are the following 81 clones.

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3013874,
 BRACE3017253, BRACE3039358, BRAMY2040915, BRAMY3015549,
 BRAWH3009961, BRAWH3023415, BRAWH3049544, BRHIP3017558,
 BRHIP3025795, BRHIP3036371, BRHIP3036715, BRHIP3038735,
 25 BRTHA2019726, BRTHA2020400, BRTHA2020721, BRTHA3017791,
 CERVX2000968, FELNG2000720, JCMLC2000273, KIDNE2004531,
 NT2RP8008057, OCBBF2000831, OCBBF2004478, OCBBF2030927,
 PEBLM2005615, PLACE7006090, SPLEN2025012, STOMA2004663,
 TESTI2021654, TESTI2052670, TESTI4008305, TESTI4022158,
 30 TESTI4031173, TESTI4032128, TESTI4037949, TESTI4051424,
 THYMU3002825, THYMU3014173, THYMU3016518, THYMU3020221,
 THYMU3025118, THYMU3026306, THYMU3026532, THYMU3037772,
 THYMU3040746, TLUNG2001445, TLUNG2001600, TRACH3003357,
 TRACH3004113, TRACH3004412, TRACH3005274, TRACH3005699,
 35 TRACH3006800, TRACH3011082, TRACH3011184, TRACH3012659,
 TRACH3015354, TRACH3018261, TRACH3018907, TRACH3019058,

TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023,
 TRACH3024512, TRACH3026299, TRACH3028441, TRACH3029670,
 TRACH3031316, TRACH3034680, TRACH3036103, TRACH3037505,
 TUTER2001433, UTERU3001946, UTERU3010409, UTERU3011398,
 5 UTERU3015647

The following two clones are also predicted to belong to the category of glycoprotein-related protein.

BRAWH3028645, TESTI4005158

The clones predicted to belong to the category of signal
 10 transduction-related protein are the following 125 clones.
 BLADE2002310, BLADE2008809, BRACE2047975, BRACE3002344,
 BRACE3003866, BRACE3004767, BRACE3013418, BRACE3015898,
 BRACE3017253, BRACE3042046, BRACE3044172, BRACE3045424,
 BRACE3046491, BRACE3051621, BRACE3052321, BRACE3052595,
 15 BRAMY3005184, BRAMY3009491, BRAMY3010321, BRAMY3014613,
 BRAMY3015547, BRAMY3017920, BRAWH2012866, BRAWH3009961,
 BRAWH3017180, BRAWH3018063, BRAWH3019026, BRAWH3022431,
 BRAWH3024186, BRAWH3026349, BRAWH3027574, BRAWH3027806,
 BRAWH3029385, BRAWH3031342, BRAWH3032340, BRAWH3035914,
 20 BRAWH3037428, BRAWH3044122, BRAWH3047692, BRCAN2000923,
 BRCAN2002892, BRCOC2001355, BRHIP3003306, BRHIP3006294,
 BRHIP3006786, BRHIP3011460, BRHIP3017109, BRHIP3021019,
 BRHIP3028570, BRHIP3037543, BRHIP3041587, BRTHA2026290,
 BRTHA2027250, BRTHA3014547, BRTHA3020771, BRTHA3021708,
 25 BRTHA3023403, BRTHA3026916, CTONG2009570, ERLTF2002369,
 FEKID2001001, FEKID2002637, FELNG2001953, KIDNE2010049,
 LYMPB2002344, N1ESE2000698, NETRP2003448, NT2RI2004818,
 NTONG2008483, OCBBF3006986, OCBBF3021086, OCBBF3021502,
 OCBBF3023175, PLACE5000492, PLACE6000055, PLACE6019600,
 30 PLACE7009936, PLACE7014247, PLACE7016526, PUAEN2006639,
 SKMUS2008585, SKMUS2009557, SMINT2017964, SPLEN2007689,
 SYNOV2017179, SYNOV4009575, TESTI4002774, TESTI4004695,
 TESTI4010902, TESTI4012960, TESTI4013474, TESTI4020342,
 TESTI4020596, TESTI4021197, TESTI4022158, TESTI4028042,
 35 TESTI4029731, TESTI4033177, TESTI4036048, TESTI4046073,
 TESTI4047808, TESTI4049786, TESTI4051865, THYMU3013785,

THYMU3025683, THYMU3032798, TRACH2024730, TRACH3003037,
 TRACH3003357, TRACH3005173, TRACH3011538, TRACH3018519,
 TRACH3020605, TRACH3024020, TRACH3030176, TRACH3031660,
 TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042,
 5 UTERU3001029, UTERU3006720, UTERU3010919, UTERU3021231,
 UTERU3022168

The following three clones are also predicted to belong to the category of signal transduction-related protein.

BRAMY3008096, TESTI4052089, TRACH3021066

10 The clones predicted to belong to the category of transcription-related protein are the following 141 clones.

ASTRO2016114, BEAST2000981, BRACE2019348, BRACE3025719,
 BRACE3026844, BRACE3026947, BRACE3029021, BRACE3034183,
 BRACE3040239, BRACE3041162, BRACE3047482, BRAMY2041347,
 15 BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027,
 BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209,
 BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3013009,
 BRAWH3013264, BRAWH3015175, BRAWH3015610, BRAWH3017477,
 BRAWH3021580, BRAWH3022651, BRAWH3027533, BRAWH3027880,
 20 BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3032571,
 BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3042787,
 BRAWH3044122, BRAWH3046424, BRCAN2021452, BRCOC2012386,
 BRHIP2027077, BRHIP2029663, BRHIP3005037, BRHIP3007609,
 BRHIP3017256, BRHIP3019824, BRHIP3027651, BRHIP3028246,
 25 BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA3000456,
 BRTHA3003225, BRTHA3010212, BRTHA3014000, BRTHA3028339,
 CHONS2000797, CTONG2006235, CTONG2011801, FCBBF3020030,
 FEBRA2002260, HCASM2008154, KIDNE2018268, NETRP2003103,
 NETRP2004017, NT2RI3009480, NTONG2003805, NTONG2008483,
 30 OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3008392,
 OCBBF3019269, OCBBF3020263, OCBBF3022827, OCBBF3025503,
 OCBBF3026361, PLACE7005169, PLACE7007973, PLACE7009757,
 PLACE7018512, SMINT2014721, SPLEN2012571, SPLEN2036608,
 T1ESE2000904, TESTI2036822, TESTI2040377, TESTI4000370,
 35 TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796,
 TESTI4003944, TESTI4005322, TESTI4005470, TESTI4024494,

TESTI4028182, TESTI4032913, TESTI4039904, TESTI4051054,
 TESTI4052775, THYMU2008207, THYMU2038199, THYMU3008105,
 THYMU3012983, THYMU3014372, THYMU3021586, THYMU3022434,
 THYMU3026000, THYMU3030072, THYMU3034671, THYMU3037617,
 5 THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616,
 TLUNG2000654, TRACH3002752, TRACH3003037, TRACH3003458,
 TRACH3004113, TRACH3004412, TRACH3004424, TRACH3005274,
 TRACH3010079, TRACH3010167, TRACH3015951, TRACH3022109,
 TRACH3026303, TRACH3028180, TRACH3036750, UTERU2037423,
 10 UTERU3012293, UTERU3015011, UTERU3016070, UTERU3018172,
 UTERU3022588

The following eight clones are also predicted to belong to the category of transcription-related protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI2046536,
 15 TESTI4002988, TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of disease-related protein are the following four clones.

BRAWH3041928, BRHIP3000859, BRTHA3018409, THYMU3025642

The clones predicted to belong to the category of enzyme
 20 and/or metabolism-related protein are the following 264 clones.

BRACE1000475, BRACE2003628, BRACE2012528, BRACE2013132,
 BRACE2016896, BRACE2035120, BRACE2042541, BRACE2047975,
 BRACE3002344, BRACE3009392, BRACE3013418, BRACE3015898,
 BRACE3017253, BRACE3019941, BRACE3024444, BRACE3031315,
 25 BRACE3031372, BRACE3032537, BRACE3033525, BRACE3034183,
 BRACE3034964, BRACE3039288, BRACE3039454, BRACE3041059,
 BRACE3042409, BRACE3044172, BRACE3046491, BRACE3049714,
 BRACE3050270, BRACE3051819, BRACE3052410, BRACE3052595,
 BRAMY3007078, BRAMY3009491, BRAMY3011581, BRAMY3014613,
 30 BRAWH4000915, BRAWH2000256, BRAWH2002333, BRAWH2012866,
 BRAWH2014053, BRAWH2016785, BRAWH3009961, BRAWH3010657,
 BRAWH3013264, BRAWH3015175, BRAWH3017180, BRAWH3017259,
 BRAWH3019026, BRAWH3021724, BRAWH3022431, BRAWH3023415,
 BRAWH3024186, BRAWH3028796, BRAWH3029385, BRAWH3029806,
 35 BRAWH3032571, BRAWH3033513, BRAWH3034668, BRAWH3034743,
 BRAWH3037979, BRAWH3041556, BRAWH3043295, BRAWH3044122,

BRAWH3044985, BRAWH3046424, BRAWH3047692, BRAWH3048724,
BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402,
BRCAN2021325, BRCOC2001355, BRCOC2006164, BRHIP2029663,
BRHIP3001481, BRHIP3002000, BRHIP3002114, BRHIP3002141,
5 BRHIP3003063, BRHIP3003126, BRHIP3003795, BRHIP3004725,
BRHIP3005307, BRHIP3005673, BRHIP3007195, BRHIP3007223,
BRHIP3011082, BRHIP3012289, BRHIP3016032, BRHIP3019643,
BRHIP3021019, BRHIP3032374, BRHIP3033557, BRHIP3035006,
BRHIP3037543, BRHIP3038030, BRHIP3041587, BRSSN2004710,
10 BRSSN2011843, BRSTN2011961, BRSTN2016918, BRTHA2001304,
BRTHA2005448, BRTHA2026290, BRTHA2026311, BRTHA2027250,
BRTHA2030036, BRTHA2033683, BRTHA2035743, BRTHA2036295,
BRTHA2037247, BRTHA3003736, BRTHA3010135, BRTHA3014547,
BRTHA3021786, BRTHA3023403, BRTHA3026916, CHONS2002829,
15 COLON2004351, CTONG2010330, CTONG2020582, CTONG2026987,
FCBBF3001018, FCBBF3021191, FEBRA2013570, FEBRA2026582,
FEHRT2002708, FEKID2002637, HHDPC2008185, HSYRA2004550,
KIDNE2004531, KIDNE2010049, LYMPB2002236, NT2RI2004818,
NT2RI3001967, NT2RP7016508, NT2RP8003490, NT2RP8003787,
20 NT2RP8005546, OCBBF2000831, OCBBF2007039, OCBBF2024589,
OCBBF3001616, OCBBF3004487, OCBBF3021086, OCBBF3023175,
OCBBF3025503, OCBBF3026088, OCBBF3026361, PLACE5000492,
PLACE6003004, PLACE7003985, PLACE7004103, PLACE7004961,
PLACE7006090, PLACE7007379, PLACE7008136, PLACE7012111,
25 PLACE7014247, PLACE7016526, SKMUS2008585, SKMUS2009557,
SMINT2011406, SMINT2011509, SYNOV2017179, SYNOV4003174,
SYNOV4009139, T1ESE2000609, T1ESE2002665, TESTI2001364,
TESTI2005112, TESTI2007490, TESTI2018335, TESTI2021112,
TESTI2021654, TESTI2030901, TESTI2037877, TESTI2049062,
30 TESTI4000621, TESTI4002774, TESTI4002799, TESTI4003404,
TESTI4003565, TESTI4003602, TESTI4003703, TESTI4005399,
TESTI4007671, TESTI4010544, TESTI4010721, TESTI4012960,
TESTI4017854, TESTI4020342, TESTI4020596, TESTI4020819,
TESTI4021129, TESTI4021197, TESTI4023096, TESTI4024494,
35 TESTI4026080, TESTI4028182, TESTI4031066, TESTI4033177,
TESTI4040598, TESTI4041482, TESTI4046073, TESTI4047808,

TESTI4049786, TESTI4051424, TESTI4051865, TESTI4052219,
 THYMU3000390, THYMU3002825, THYMU3014372, THYMU3023400,
 THYMU3025683, THYMU3026306, THYMU3026479, THYMU3031878,
 THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428,
 5 THYMU3047115, THYMU3047891, TRACH2022113, TRACH2024730,
 TRACH3003037, TRACH3005274, TRACH3006800, TRACH3009008,
 TRACH3009061, TRACH3011313, TRACH3016455, TRACH3017409,
 TRACH3018108, TRACH3018261, TRACH3019621, TRACH3021544,
 TRACH3023516, TRACH3024020, TRACH3024081, TRACH3024342,
 10 TRACH3024512, TRACH3025316, TRACH3026303, TRACH3026650,
 TRACH3027229, TRACH3027701, TRACH3029329, TRACH3032150,
 TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042,
 UTERU3001946, UTERU3010604, UTERU3010919, UTERU3015299,
 UTERU3017441, UTERU3019708, UTERU3020090, UTERU3022168

15 The following seven clones are also predicted to belong to
 the category of enzyme and/or metabolism-related protein.

ADRGL2011190, BRAMY3008096, CTONG2002832, TESTI4052089,
 THYMU3024602, THYMU3044175, TRACH3021066

The clones predicted to belong to the category of cell
 20 division and/or cell proliferation-related protein are the
 following 13 clones.

BRACE3022303, BRAWH3017260, BRHIP2008756, BRHIP3028570,
 BRSTN2006638, NT2RI2004818, PLACE7009563, PLACE7016526,
 SMINT2014721, THYMU3025642, THYMU3033626, TRACH3029329,
 25 UTERU3010919

The following one clone is also predicted to belong to the
 category of cell division and/or cell proliferation-related
 protein.

TBAES2007481

30 The clones predicted to belong to the category of
 cytoskeleton-related protein are the following 51 clones.

BRACE2046976, BRACE3013874, BRACE3047482, BRACE3051819,
 BRAMY3015549, BRAWH3015175, BRAWH3018548, BRAWH3021580,
 BRAWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3032298,
 35 BRAWH3049544, BRHIP3003340, BRHIP3012736, BRHIP3036936,
 BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA2031917,

BRTHA3011361, BRTHA3025073, CTONG2008989, HSYRA2007338,
 LYMPB2002458, OCBBF3008835, OCBBF3027969, PEBLM2006298,
 PLACE7000266, PLACE7004103, PLACE7004961, SMINT2011406,
 SYNOV4003174, TESTI2006543, TESTI2034913, TESTI4001517,
 5 TESTI4005653, TESTI4008305, TESTI4041049, TESTI4051424,
 TESTI4051865, THYMU3020221, THYMU3038158, TLUNG2000654,
 TRACH3002890, TRACH3006379, TRACH3012460, TRACH3018524,
 TRACH3020769, TRACH3028837, UTERU3011837

10 The clones predicted to belong to the category of nuclear
 protein and/or RNA synthesis-related protein are the following
 29 clones.

BRACE2016896, BRACE3032537, BRACE3034183, BRACE3039288,
 BRAWH3013264, BRAWH3032571, BRCOC2006164, BRHIP3004725,
 BRSSN2011843, BRTHA2026290, BRTHA3003736, BRTHA3014547,
 15 NT2RP7016508, NT2RP8005546, OCBBF3004487, OCBBF3021086,
 OCBBF3026361, PLACE5000492, TESTI4000621, TESTI4002799,
 TESTI4010721, TESTI4012960, THYMU3014372, THYMU3033626,
 THYMU3041428, TRACH3017409, TRACH3029462, UTERU3010919,
 UTERU3019708

20 The clones predicted to belong to the category of protein
 synthesis and/or transport-related protein are the following 50
 clones.

BRACE3033525, BRACE3041059, BRAMY4001652, BRAWH3010657,
 BRAWH3013264, BRAWH3034668, BRAWH3036247, BRAWH3037428,
 25 BRAWH3037979, BRCAN2000923, BRCAN2002892, BRCAN2006051,
 BRCAN2021325, BRCAN2021718, BRHIP2029663, BRHIP3002000,
 BRHIP3003126, BRHIP3007223, BRHIP3011082, BRSTN2010089,
 BRTHA2036295, BRTHA3012265, CHONS2002829, D9OST2004417,
 HHDPC2008185, NETRP2003448, OCBBF2007039, OCBBF3021086,
 30 PLACE6003004, PLACE6010925, PLACE7006498, PLACE7007379,
 PLACE7012111, PLACE7016526, TESTI2023903, TESTI2036285,
 TESTI4003602, TESTI4012960, TESTI4014415, TESTI4030864,
 TESTI4051865, THYMU3036953, THYMU3047891, TRACH3004113,
 TRACH3006800, TRACH3009061, TRACH3021544, TRACH3026650,
 35 UTERU3001946, UTERU3012414

The following one clone is also predicted to belong to the category of protein synthesis and/or transport-related protein.

CTONG2002832

The clones predicted to belong to the category of cellular defense-related protein are the following four clones.

BRHIP3027191, SYNOV4009575, TESTI2023903, TRACH3029462

The clone predicted to belong to the category of development and/or differentiation-related protein is the following one clone.

10 CHONS2000797

The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 185 clones.

ASTRO2016114, BEAST2000981, BRACE2012625, BRACE2016896,
BRACE2019348, BRACE3019941, BRACE3025719, BRACE3026844,
15 BRACE3026947, BRACE3029021, BRACE3031743, BRACE3032537,
BRACE3034183, BRACE3039288, BRACE3040239, BRACE3041162,
BRACE3047482, BRACE3050270, BRALZ2013621, BRAMY2041347,
BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027,
BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209,
20 BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3011623,
BRAWH3013009, BRAWH3013264, BRAWH3015175, BRAWH3015610,
BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAWH3027533,
BRAWH3027607, BRAWH3027880, BRAWH3028796, BRAWH3031342,
BRAWH3031710, BRAWH3032571, BRAWH3035403, BRAWH3035936,
25 BRAWH3036247, BRAWH3036334, BRAWH3038055, BRAWH3042787,
BRAWH3044122, BRCAN2020331, BRCAN2021452, BRCOC2006164,
BRCOC2012386, BRHIP2027077, BRHIP2029663, BRHIP3002141,
BRHIP3004725, BRHIP3005037, BRHIP3007609, BRHIP3017256,
BRHIP3019824, BRHIP3027651, BRHIP3028246, BRHIP3039592,
30 BRSSN2011843, BRSTN2012069, BRTHA2026290, BRTHA2037247,
BRTHA3000456, BRTHA3003225, BRTHA3003736, BRTHA3010212,
BRTHA3014000, BRTHA3014547, BRTHA3028339, CHONS2000797,
CTONG2003517, CTONG2006235, CTONG2011801, CTONG2026987,
D9OST2003106, FCBBF3020030, FEBRA2002260, FEBRA2028457,
35 FEHRT2002708, HCASM2008154, KIDNE2018268, NETRP2003103,
NETRP2004017, NT2RI3009480, NT2RP7016508, NT2RP8005546,

NTONG2003805, NTONG2008483, OCBBF2014745, OCBBF2016928,
 OCBBF3001333, OCBBF3001616, OCBBF3004487, OCBBF3008392,
 OCBBF3019269, OCBBF3020263, OCBBF3021086, OCBBF3021361,
 OCBBF3022827, OCBBF3025503, OCBBF3026361, PLACE5000492,
 5 PLACE7004103, PLACE7005169, PLACE7007973, PLACE7008136,
 PLACE7009757, PLACE7018512, PROST2002078, SMINT2011509,
 SMINT2014721, SPLEN2012571, SPLEN2036608, TIESE2000609,
 TIESE2000904, TESTI2036822, TESTI2040377, TESTI4000370,
 TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796,
 10 TESTI4003944, TESTI4005322, TESTI4005470, TESTI4012960,
 TESTI4024494, TESTI4028182, TESTI4032913, TESTI4039904,
 TESTI4051054, TESTI4052775, THYMU2008207, THYMU2038199,
 THYMU3008105, THYMU3012983, THYMU3014372, THYMU3021586,
 THYMU3022434, THYMU3023400, THYMU3026000, THYMU3030072,
 15 THYMU3037617, THYMU3040829, THYMU3041428, THYMU3043200,
 THYMU3045704, TKIDN2003396, TLIVE2001616, TLUNG2000654,
 TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113,
 TRACH3004412, TRACH3004424, TRACH3005274, TRACH3010079,
 TRACH3010167, TRACH3015951, TRACH3017409, TRACH3021778,
 20 TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750,
 UTERU2037423, UTERU3012293, UTERU3015011, UTERU3016070,
 UTERU3019708, UTERU3020090, UTERU3022168, UTERU3022588,
 UTERU3023141

The following seven clones are also predicted to belong to
 25 the category of DNA-binding and/or RNA-binding protein.

BRACE3002184, BRCAN2019772, CTONG2002832, TESTI4002988,
 TESTI4005500, TRACH1000193, TRACH3019290

The clones predicted to belong to the category of ATP
 binding and/or GTP-binding protein are the following 41 clones.

30 BRACE3042409, BRAWH2002333, BRAWH2014053, BRAWH3015175,
 BRAWH3029385, BRAWH3029806, BRAWH3034743, BRAWH3037428,
 BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2022126,
 BRCOC2001355, BRCOC2006164, BRHIP3007195, BRSSN2004710,
 BRTHA2026290, BRTHA2033683, BRTHA3026916, CTONG2020582,
 35 HSYRA2004550, NETRP2003448, PLACE6019600, PLACE7004961,
 PLACE7006498, PLACE7016526, SMINT2011406, TESTI4010544,

TESTI4014415, TESTI4028182, TESTI4029731, TESTI4040559,
 TESTI4041482, TESTI4052219, THYMU3013785, THYMU3047115,
 TRACH2024730, TRACH3024081, TRACH3029329, TRACH3031660,
 UTERU3012414

- 5 The following one clone is also predicted to belong to the
 category of ATP binding and/or GTP-binding protein.

ADRGL2011190

- 10 Although the 172 clones described below have hit data in
 Pfam, it remains unclear as to which of the above-described
 categories each of these clones belong. However, if data for
 proteins having a similar domain or motif are accumulated and
 their functions clarified in more detail, in the future these
 clones can be classified into any of the above-described
 categories. The Clone Name and Functional Domain Name are
 15 indicated as "Clone Name//Functional Domain Name". When a clone
 had hit data in multiple functional domains, all data were
 represented, with each marked with a double slash (/).

- 20 In addition, even when a clone had multiple hit data in an
 identical functional domain, these data are fully represented
 without abridgment.

- BLADE2001031// Thrombospondin type 1 domain
 BRACE2010336// TPR Domain
 BRACE2013009// EF hand
 BRACE2017872// PWWP domain
 25 BRACE2023744// Translationally controlled tumor protein
 BRACE2034434// Protein of unknown function
 BRACE3001973// EGF-like domain//Laminin G domain
 BRACE3002756// SAM domain (Sterile alpha motif)
 BRACE3005903// K-box region//TSC-22/dip/bun family
 30 BRACE3014523// Wiskott Aldrich syndrome homology region 2
 BRACE3019570// Troponin
 BRACE3022340// Troponin
 BRACE3026345// Insulin/IGF/Relaxin family
 BRACE3036283// DnaJ domain
 35 BRACE3040644// Low-density lipoprotein receptor domain class
 A//EB module//CUB domain

BRACE3043597// KOW motif
 BRACE3046466// EGF-like domain//Laminin G domain//Laminin EGF-like (Domains III and V)//EB module
 BRACE3048615// Leucine Rich Repeat
 5 BRALZ2010842// Mitochondrial carrier proteins
 BRAMY2031516// wnt family of developmental signaling proteins
 BRAMY2041384// Annexin
 BRAMY3002886// Domain of unknown function//CBS domain
 BRAMY3011501// SAP domain//SPRY domain
 10 BRAMY3015086// FERM domain (Band 4.1 family)
 BRAMY3018754// Protein of unknown function//Domain of unknown function
 BRAMY4000962// Tudor domain
 BRAWH2011796// S-100/ICaBP type calcium binding domain//EF hand
 15 BRAWH2016223// TPR Domain
 BRAWH3001783// Cadherin domain
 BRAWH3003573// EF hand
 BRAWH3008167// Sushi domain (SCR repeat)//CUB domain
 BRAWH3011331// Disintegrin
 20 BRAWH3011577// KRAB box
 BRAWH3014609// Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine rich repeat C-terminal domain
 BRAWH3021574// Wiskott Aldrich syndrome homology region 2
 BRAWH3022347// Leucine Rich Repeat
 25 BRAWH3022719// Eukaryotic initiation factor 4E
 BRAWH3024231// TPR Domain
 BRAWH3026938// PDZ domain (Also known as DHR or GLGF).
 BRAWH3027440// TPR Domain//PPR repeat
 BRAWH3030772// Ank repeat
 30 BRAWH3030910// SAM domain (Sterile alpha motif)
 BRAWH3033448// TPR Domain
 BRAWH3034775// SAP domain//SPRY domain
 BRAWH3038252// Formin Homology 2 Domain
 BRAWH3038324// Dehydrins
 35 BRAWH3038827// Kelch motif//BTB/POZ domain
 BRAWH3042438// 'Paired box' domain//EF hand//Phorbol

esters/diacylglycerol binding domain (C1 domain)
 BRAWH3042568// Homeobox domain
 BRAWH3044151// Thrombospondin type 1 domain//Keratin, high
 sulfur B2 protein
 5 BRAWH3045118// DnaJ domain
 BRAWH3048374// Sushi domain (SCR repeat)//Keratin, high sulfur
 B2 protein
 BRCAN2010665// PDZ domain (Also known as DHR or GLGF).
 BRCAN2019907// EF hand
 10 BRCAN2020234// Lipocalin / cytosolic fatty-acid binding protein
 family
 BRCAN2025093// Ank repeat//Flagellar FliJ protein
 BRCOC2006639// Leucine Rich Repeat
 BRHIP2013958// Domain of unknown function//MSP (Major sperm
 15 protein) domain
 BRHIP2026346// Formin Homology 2 Domain
 BRHIP2027563// Kelch motif
 BRHIP3001878// POT family
 BRHIP3004710// TPR Domain
 20 BRHIP3005142// Adaptin N terminal region
 BRHIP3005231// TPR Domain
 BRHIP3006449// Armadillo/beta-catenin-like repeats
 BRHIP3007424// wnt family of developmental signaling proteins
 BRHIP3009753// CUB domain//Low-density lipoprotein receptor
 25 domain class A
 BRHIP3010289// Delta serrate ligand//Kelch motif//Plexin
 repeat//Lectin C-type domain//Laminin EGF-like (Domains III and
 V)//Keratin, high sulfur B2 protein
 BRHIP3020733// Keratin, high sulfur B2 protein
 30 BRHIP3029409// NTR/C345C module
 BRHIP3030230// Pentaxin family
 BRHIP3033734// Keratin, high sulfur B2 protein
 BRSSN2015497// Tudor domain
 BRTHA2038345// Ank repeat
 35 BRTHA3011187// EF hand
 BRTHA3021971// Putative peptidoglycan binding domain

BRTHA3026161// Adenosine-deaminase (editase) domain
 BRTHA3027171// Scorpion short toxins
 BRTHA3027638// Matrix protein (MA), p15
 CHONS2001287// Insulin-like growth factor binding
 5 proteins//Thyroglobulin type-1 repeat
 CHONS2001834// Plexin repeat
 DFNES2011221// Rotavirus NS26
 ERLTF2002178// Kelch motif
 FCBBF3012443// Leucine rich repeat N-terminal domain//Leucine
 10 Rich Repeat//Leucine rich repeat C-terminal domain
 FCBBF3024911// PWWP domain
 FCBBF5000384// BAF60b domain of the SWIB complex
 FEBRA2000805// Uncharacterized protein family UPF0054
 FEBRA2023498// Leucine rich repeat N-terminal domain//Leucine
 15 Rich Repeat
 FEKID2002493// wnt family of developmental signaling proteins
 HCHON2009766// eIF4-gamma/eIF5/eIF2-epsilon
 JCMCLC2002751// von Willebrand factor type D domain//Plant PEC
 family metallothionein//Trypsin Inhibitor like cysteine rich
 20 domain//von Willebrand factor type C domain
 KIDNE2015987// EGF-like domain//Keratin, high sulfur B2
 protein//Zona pellucida-like domain
 NT2RI3001573// Leucine Rich Repeat
 NT2RI3005923// Cadherin domain
 25 NT2RI3009524// EGF-like domain//Metallothionein//Laminin G
 domain
 NT2RP7007387// Armadillo/beta-catenin-like repeats//picornavirus
 capsid protein
 NT2RP7020343// Transforming growth factor beta like
 30 domain//Keratin, high sulfur B2 protein
 NT2RP8000633// VPR/VPX protein
 NT2RP8001604// CUB domain//Sushi domain (SCR repeat)
 NT2RP8006452// African swine fever virus multigene family 360
 protein//Leucine Rich Repeat
 35 NT2RP8007920// PPR repeat//LIM domain containing proteins
 NT2RP8009119// Picornavirus 2B protein

OCBBF3001202// DENN (AEX-3) domain
 OCBBF3005330// Domain found in Dishevelled, Egl-10, and
 Pleckstrin//TCP-1/cpn60 chaperonin family
 OCBBF3023913// R3H domain//Retroviral Vif (Viral infectivity)
 5 protein
 OCBBF3026979// Laminin G domain//Thrombospondin N-terminal -like
 domains//von Willebrand factor type C domain//EGF-like
 domain//EB module//Plant PEC family metallothionein//Trypsin
 Inhibitor like cysteine rich domain//Metallothionein
 10 PEBLM2001803// Vacuolar sorting protein 9 (VPS9) domain
 PLACE6001933// Receptor L domain
 PLACE7002303// Homeobox domain
 PUAEN2000594// Poly-adenylate binding protein, unique domain.
 PUAEN2000684// Geminivirus AL2 protein//Leucine Rich Repeat
 15 SMINT2010753// TPR Domain//PPR repeat
 SPLEN2022785// Polyomavirus coat protein
 SPLEN2028417// Homeobox domain
 SYNOV2003326// TSC-22/dip/bun family
 TBAES2003917// Ank repeat
 20 TBAES2007428// Scorpion short toxins//EGF-like domain
 TESOP2002005// E7 protein, Early protein
 TESTI2005564// EF hand
 TESTI2009739// Tropomyosins//Domain of unknown function
 TESTI2011020// Keratin, high sulfur B2 protein
 25 TESTI2018867// FF domain
 TESTI2049041// TPR Domain
 TESTI4001569// Leucine Rich Repeat//KE2 family protein
 TESTI4002141// Keratin, high sulfur B2 protein
 TESTI4002868// Metallothionein
 30 TESTI4004031// Domain of unknown function
 TESTI4007965// Adaptin N terminal region//Gamma-adaptin, C-
 terminus
 TESTI4011926// Gag P30 core shell protein
 TESTI4013742// Leucine Rich Repeat//Hantavirus nucleocapsid
 35 protein//Troponin//Formin Homology 2 Domain//Apolipoprotein
 A1/A4/E family

TESTI4024294// Chorion protein
 TESTI4035898// Kelch motif
 TESTI4039451// Adaptin N terminal region
 TESTI4041984// EGF-like domain//EB module//TB domain
 5 TESTI4043166// Formin Homology 2 Domain
 TESTI4046873// TPR Domain
 TESTI4047328// von Willebrand factor type D domain//Trypsin
 Inhibitor like cysteine rich domain//Chitin binding
 domain//Metallothionein
 10 TESTI4047569// Keratin, high sulfur B2 protein
 TESTI4051015// Major intrinsic protein
 TESTI4052598// Lectin C-type domain
 THYMU3003007// TPR Domain
 THYMU3012402// Armadillo/beta-catenin-like repeats
 15 THYMU3015042// Polyomavirus coat protein
 THYMU3015571// Chaperonins 10 Kd subunit
 THYMU3017761// Gag P30 core shell protein
 THYMU3019476// Matrix protein (MA), p15
 THYMU3021755// HCO3- transporter family
 20 THYMU3033649// Immunoreceptor tyrosine-based activation motif
 THYMU3040126// Metallothionein
 THYMU3046360// F-box domain.
 TKIDN2011051// Keratin, high sulfur B2 protein
 TKIDN2011160// Thrombospondin type 1 domain
 25 TLIVE2007736// PDZ domain (Also known as DHR or GLGF).
 TRACH3007689// Ank repeat//TPR Domain
 TRACH3012106// FERM domain (Band 4.1 family)
 TRACH3015346// Uncharacterized protein family UPF0004
 TRACH3016805// Ank repeat
 30 TRACH3018606// SAM domain (Sterile alpha motif)
 TRACH3022296// DnaJ domain
 TRACH3022758// EF hand
 TRACH3023203// Flavivirus polyprotein propeptide
 TRACH3028855// R3H domain//Uncharacterized protein family
 35 UPF0024
 TRACH3030855// Serpins (serine protease inhibitors)

TRACH3032570// PDZ domain (Also known as DHR or GLGF).

UTERU2016669// Helix-hairpin-helix motif.

UTERU3001394// EGF-like domain

UTERU3009775// PDZ domain (Also known as DHR or GLGF).

5 UTERU3011558// GTPase of unknown function

UTERU3011579// Plant PEC family metallothionein

UTERU3017995// UBX domain

UTERU3018255// Thrombospondin type 1 domain

UTERU3021850// Thrombospondin type 1 domain//DnaJ central domain

10 (4 repeats)

Likewise, although seven clones described below have hit data in Pfam (see Example 5), it remains unclear as to which of the above-described categories each of the clones belong. However, if data for proteins comprising a similar domain or motif are accumulated and their functions are clarified in more detail, in the future these clones can be classified into any of the categories described above.

BRACE3026993// TSC-22/dip/bun family

BRACE3046450// PDZ domain (Also known as DHR or GLGF).//PDZ

20 domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF). 1//PDZ domain (Also known as DHR or GLGF).

CTONG2003764// Phorbol esters/diacylglycerol binding domain (C1 domain)

TBAES2004105// Thrombospondin type 1 domain

25 TBAES2007379// EGF-like domain//EGF-like domain//Trypsin

Inhibitor like cysteine rich domain//EGF-like domain//EGF-like domain//Keratin, high sulfur B2 protein//EGF-like domain//EGF-like domain//Granulins//EGF-like domain//EGF-like domain//EGF-like domain

30 TBAES2008133// PDZ domain (Also known as DHR or GLGF).

UTERU2036507// Thrombospondin type 1 domain//NTR/C345C module

In addition, when data for proteins are accumulated and novel domains and motifs are found, in the future the remaining clones, which had no hit data in the search with Pfam, can be classified into any of the above-described categories if a new functional domain or motif is identified by re-analyzing the

35

deduced amino acid sequences of the clones using a homology search against an updated database.

EXAMPLE 8

5 Expression frequency analysis in silico

The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data.
10 The database was constructed based on the nucleotide sequences of 1,402,069 clones, and thus the population of the database is large enough for the analysis.

Then, clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide
15 sequences of respective clones in this database with the program of nucleotide sequence homology search; the number of clones belonging to each cluster was determined and normalized for every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of
20 the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a
25 tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more
30 cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 2 to 24 shown below represents a relative expression frequency; the higher the value, the higher the expression level. The genes which are
35 included a part of the Tables indicate not so big difference between compared libraries, but when compared with other

libraries from another tissue or cell based on Example 9, they indicate significant difference. Thus, the genes are specific in each tissue or cell, and can be considered to be useful as diagnosing markers for the disease as well as useful for
 5 analyzing molecular mechanisms.

Osteoporosis-related genes

Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The
 10 onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648.
 15 (2001)) are genes involved in osteoporosis relevant to bone metabolism.

A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a
 20 glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from
 25 the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following twelve clones (Table 2).

30 BRAWH3018063, BRHIP3020046, BRSSN2013696, BRSTN2012069, BRTHA2027229, D9OST2003106, D9OST2003989, D9OST2004417, OCBBF2016928, TESTI4005653, TESTI4013474, THYMU3032798

These genes are involved in osteoporosis.

35 Genes involved in neural cell differentiation

Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2.

The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following 102 clones (Table 3).

BLADE2004849, BRACE2003628, BRACE2012528, BRAMY2023939, BRAMY2031516, BRAMY4002628, BRAWH3010461, BRAWH3017259, BRAWH3018063, BRAWH3022651, BRAWH3024186, BRCAN2019653, BRCAN2022126, BRCOC2012386, BRHIP3002000, BRHIP3007223, BRHIP3021019, BRSTN2011961, BRSTN2012069, BRTHA2033155, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3021971, CHONS2002829, CTONG2006235, FCBBF3012443, FEBRA2026582, LIVER2008465, NT2NE2011107, NT2NE2016041, NT2RI2004818, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI2023671, NT2RI2028537, NT2RI3001573, NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3007095, NT2RI3008179, NT2RI3009480, NT2RI3009524, NT2RP7003439, NT2RP7007387, NT2RP7014178, NT2RP7014778, NT2RP7016508, NT2RP7017139, NT2RP7019682, NT2RP7020343, NT2RP8000633, NT2RP8001363, NT2RP8001407, NT2RP8001584, NT2RP8001604, NT2RP8001605, NT2RP8003490, NT2RP8003657, NT2RP8003787, NT2RP8005546, NT2RP8006452, NT2RP8006521, NT2RP8007416, NT2RP8007503, NT2RP8007920, NT2RP8008057, NT2RP8009119, NT2RP8009248, NTONG2008483, OCBBF2003518, OCBBF3001333, OCBBF3004908, PLACE7004103, PROST2017910, SMINT2009292, SPLEN2012571, T1ESE2000904, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4005653, TESTI4007965, TESTI4012960, TESTI4018436,

THYMU3001776, THYMU3002887, THYMU3029795, THYMU3041428,
 THYMU3047115, TRACH3003872, TRACH3004424, TRACH3006717,
 TRACH3007625, TRACH3009008, TRACH3016805, TRACH3016885,
 TRACH3026303, UTERU2016669

5 These genes are neurological disease-related genes.

Genes involved in Alzheimer's disease

Alzheimer's disease is a cranial neurological disease that
 is characterized by memory loss. As the disease advances,
 10 patients can no longer support themselves and require nursing.
 Alzheimer's disease eventually leads to atrophication of the
 brain itself. Environmental factors such as stress, and
 vascular factors such as hypertension and cholesterolemia, are
 assumed, but not confirmed, to contribute to the onset of
 15 Alzheimer's disease. Genes whose expression levels differ
 between normal brain tissues and tissues affected with
 Alzheimer's disease are expected to be involved in Alzheimer's
 disease. Such genes can be used to elucidate the disease's
 onset mechanism and in genetic diagnosis. cDNA libraries
 20 derived from the cerebral cortex of Alzheimer patients (BRALZ
 and BRASW), and a library derived from whole tissues of a normal
 brain (BRAWH) were analyzed and compared (Table 4). The results
 showed that genes whose expression levels differed between the
 two are the following 298 and five clones listed below.

25 ASTRO2016114, BRACE2002392, BRACE2012528, BRACE3004371,
 BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031743,
 BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863,
 BRACE3042432, BRACE3045981, BRALZ2003119, BRALZ2007661,
 BRALZ2008930, BRALZ2010842, BRALZ2011337, BRALZ2013621,
 30 BRALZ2013690, BRALZ2014054, BRAMY2031516, BRAMY3002329,
 BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAWH2000256,
 BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619,
 BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054,
 BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209,
 35 BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562,
 BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053,

BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244,
BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350,
BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896,
BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961,
5 BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726,
BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402,
BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907,
BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779,
BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508,
10 BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175,
BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715,
BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477,
BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548,
BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594,
15 BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884,
BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580,
BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347,
BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651,
BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168,
20 BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186,
BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989,
BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440,
BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616,
BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202,
25 BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796,
BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806,
BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054,
BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340,
BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448,
30 BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134,
BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890,
BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936,
BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334,
BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428,
35 BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230,
BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2019653,

BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153,
 BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3003063,
 BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409,
 BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784,
 5 BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSTN2010089,
 BRSTN2012069, BRSTN2016992, BRTHA2033155, BRTHA3003736,
 BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194,
 BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971,
 BRTHA3023403, CTONG2006235, CTONG2009033, CTONG2020582,
 10 D9OST2003106, DFNES2001829, KIDNE2010049, MESAN2017133,
 NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524,
 NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483,
 OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487,
 PLACE7004103, PLACE7006240, PROST2007444, PROST2017910,
 15 TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072,
 TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210,
 TESTI4005399, TESTI4005653, TESTI4006441, TESTI4013474,
 TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887,
 THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306,
 20 THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827,
 THYMU3038214, THYMU3041428, THYMU3044075, TRACH2013585,
 TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424,
 TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632,
 TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885,
 25 TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676,
 TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399,
 UTERU3010409, UTERU3013167
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 TRACH1000193

30 These genes are involved in Alzheimer's disease.

Genes involved in Parkinson's disease

Parkinson's disease is a cranial neurological disease
 characterized by impaired production of the neurotransmitter
 dopamine in the substantia nigra in the brain. This results in
 35 dyskinesia, such as hand tremors, and impaired body movement due
 to muscular rigidity. Normally, the number of brain neurons

gradually decreases with age. However, compared to healthy people, patients with Parkinson's disease experience a rapid and marked decrease in the number of neurons in their substantia nigra. Genes whose expression levels differ between tissues of the whole brain and the nigra are expected to be involved in Parkinson's disease. These genes exhibit nigra-specific alterations in their expression levels, and can be used to elucidate the disease onset mechanism and in gene diagnosis. cDNA libraries derived from the substantia nigra (BRSSN) and a library derived from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 5). Genes whose expression levels differed between the two were the 305 clones and five clones listed below.

ASTRO2016114, BRACE2012528, BRACE2017844, BRACE3004371,
 BRACE3004767, BRACE3022340, BRACE3025719, BRACE3026802,
 BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631,
 BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981,
 BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912,
 BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078,
 BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812,
 BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,
 BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305,
 BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,
 BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,
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 BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886,
 BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559,
 BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602,
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 BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
 BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005,
 BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,
 BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639,
 BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825,
 BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
 BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063,

BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200,
BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012,
BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
5 BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459,
BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274,
BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242,
BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
10 BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574,
BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461,
BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385,
BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
15 BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743,
BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
20 BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247,
BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979,
BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324,
BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386,
25 BRHIP2015153, BRHIP2027077, BRHIP2029643, BRHIP3001573,
BRHIP3002000, BRHIP3003063, BRHIP3003984, BRHIP3004774,
BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675,
BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019,
BRHIP3028246, BRHIP3028570, BRSSN2004303, BRSSN2004710,
30 BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198,
BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2010089,
BRSTN2011961, BRSTN2012069, BRSTN2016992, BRSTN2017104,
BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135,
BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791,
35 BRTHA3020771, BRTHA3021971, BRTHA3023403, CTONG2006235,
CTONG2009033, CTONG2011801, CTONG2020582, D9OST2003106,

DFNES2001829, KIDNE2010049, MESAN2017133, NT2RI2009233,
 NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
 NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518,
 OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103,
 5 PLACE7006240, PROST2007444, SMINT2009292, T1ESE2000904,
 TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072,
 TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210,
 TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908,
 TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350,
 10 THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
 THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214,
 THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037,
 TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,
 TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079,
 15 TRACH3016805, TRACH3016885, TRACH3022198, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,
 TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
 UTERU3013167
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 20 TRACH1000193

These genes are involved in Parkinson's disease.

Genes involved in short-term memory and dementia

In the brain, the hippocampus is a highly important memory-
 25 related area. The hippocampus functions to establish a memory
 by judging whether acquired information is necessary, and then
 accumulating the memory in another area of the brain. According
 to clinical findings, patients can retain a new memory for only
 about five minutes with an abnormal, or at the worst without a
 30 hippocampus. Some dementia patients are presumed to have
 hippocampus abnormalities. Thus, genes whose expression levels
 differ between tissues of the whole brain and the hippocampus
 are expected to be involved in memory or dementia. Such genes
 can be used to elucidate the mechanism underlying the memory and
 35 in gene diagnosis. cDNA libraries derived from the hippocampus
 (BRHIP) and from the whole tissues of a normal brain (BRAWH)

were analyzed and compared (Table 6). Genes whose expression levels differed between the two were the 438 clones and five clones listed below.

ASTRO2016114, BRACE2002392, BRACE2012528, BRACE2017359,
 5 BRACE2017397, BRACE2017844, BRACE3004046, BRACE3004371,
 BRACE3004767, BRACE3009416, BRACE3022340, BRACE3027931,
 BRACE3029021, BRACE3031185, BRACE3031743, BRACE3032385,
 BRACE3032631, BRACE3036156, BRACE3039358, BRACE3040863,
 BRACE3042326, BRACE3042432, BRACE3045078, BRACE3045981,
 10 BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005184,
 BRAMY3005912, BRAMY3007078, BRAMY3008436, BRAMY4000915,
 BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364,
 BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958,
 BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053,
 15 BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514,
 BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884,
 BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833,
 BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335,
 BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892,
 20 BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867,
 BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657,
 BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331,
 BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685,
 BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662,
 25 BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264,
 BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017,
 BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123,
 BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260,
 BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369,
 30 BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529,
 BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318,
 BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574,
 BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724,
 BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542,
 35 BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156,
 BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421,

BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506,
BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420,
BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607,
BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880,
5 BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754,
BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538,
BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910,
BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298,
BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293,
10 BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114,
BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775,
BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914,
BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270,
BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394,
15 BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055,
BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665,
BRCAN2019953, BRCAN2022126, BRCAN2025093, BRCOC2012386,
BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177,
BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125,
20 BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735,
BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563,
BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626,
BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338,
BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878,
25 BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141,
BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931,
BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340,
BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845,
BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710,
30 BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037,
BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673,
BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294,
BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172,
BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409,
35 BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082,
BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753,

BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269,
BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185,
BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997,
BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675,
5 BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109,
BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855,
BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880,
BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733,
BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656,
10 BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795,
BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160,
BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246,
BRHIP3028570, BRHIP3028742, BRSTN2010089, BRSTN2012069,
BRSTN2016992, BRTHA2001953, BRTHA2008502, BRTHA2031517,
15 BRTHA2033155, BRTHA2035743, BRTHA3003417, BRTHA3003736,
BRTHA3005988, BRTHA3007662, BRTHA3010135, BRTHA3010212,
BRTHA3011194, BRTHA3011265, BRTHA3012265, BRTHA3017791,
BRTHA3020771, BRTHA3021971, BRTHA3023403, CHONS2002829,
CTONG2006235, CTONG2009033, CTONG2020582, D9OST2003106,
20 DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133,
NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920,
NTONG2008483, OCBBF2000831, OCBBF2003518, OCBBF2018618,
OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240,
25 PROST2007444, SMINT2012179, SYNOV4004210, TBAES2007428,
TESTI2005112, TESTI2005564, TESTI2021654, TESTI4001569,
TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602,
TESTI4003703, TESTI4003944, TESTI4004210, TESTI4005399,
TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158,
30 TESTI4029297, THYMU3000776, THYMU3002887, THYMU3003007,
THYMU3003350, THYMU3007308, THYMU3008105, THYMU3021586,
THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798,
THYMU3032867, THYMU3034671, THYMU3037827, THYMU3038214,
THYMU3044075, TKIDN2000319, TRACH2013585, TRACH3002752,
35 TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717,
TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008,

TRACH3010079, TRACH3016805, TRACH3016885, TRACH3022198,
 TRACH3024342, TRACH3024671, TRACH3025316, TRACH3026303,
 TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932,
 TRACH3038399, TSTOM2000235, UTERU3005422, UTERU3010409,
 5 UTERU3013167, UTERU3016273
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 TRACH1000193

These genes are involved in memory and dementia.

10 Genes involved in equilibrium sense and movement function

The cerebellum is the center of equilibrium sense, muscular movement, and motor learning. This area is thought to be involved in motor control, and smooth movements are achieved unconsciously due to cerebellum action. Recent studies have
 15 elucidated that the cerebellum participates in not only simple movements but also in establishing higher-order movements such as reading and writing. Thus, genes whose expression levels differ between tissues of the whole brain and the cerebellum are expected to be involved in equilibrium sense or motor function,
 20 which can be useful for elucidating the molecular mechanism controlled by the brain. cDNA libraries derived from the cerebellum (BRACE) and from the whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 7). Genes whose expression levels differed between the two were the 502 clones
 25 and nine clones listed below.

ASTRO2016114, BRACE1000475, BRACE2002392, BRACE2003628,
 BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625,
 BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947,
 BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896,
 30 BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844,
 BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633,
 BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312,
 BRACE2027382, BRACE2028956, BRACE2030039, BRACE2032584,
 BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191,
 35 BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976,
 BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973,

BRACE3002344, BRACE3002541, BRACE3002756, BRACE3003866,
BRACE3004046, BRACE3004371, BRACE3004767, BRACE3004887,
BRACE3004981, BRACE3005870, BRACE3005903, BRACE3006553,
BRACE3007649, BRACE3007869, BRACE3009075, BRACE3009265,
5 BRACE3009392, BRACE3009416, BRACE3009539, BRACE3010702,
BRACE3011447, BRACE3011774, BRACE3013418, BRACE3013874,
BRACE3013986, BRACE3014523, BRACE3014714, BRACE3015090,
BRACE3015898, BRACE3016020, BRACE3016167, BRACE3016580,
BRACE3016788, BRACE3016810, BRACE3016862, BRACE3017253,
10 BRACE3018083, BRACE3019570, BRACE3019611, BRACE3019817,
BRACE3019941, BRACE3020356, BRACE3020669, BRACE3021430,
BRACE3021517, BRACE3021805, BRACE3022051, BRACE3022303,
BRACE3022312, BRACE3022340, BRACE3022847, BRACE3023604,
BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024537,
15 BRACE3024879, BRACE3025627, BRACE3025719, BRACE3026161,
BRACE3026290, BRACE3026345, BRACE3026456, BRACE3026802,
BRACE3026844, BRACE3026947, BRACE3027256, BRACE3027931,
BRACE3028360, BRACE3028895, BRACE3028998, BRACE3029005,
BRACE3029021, BRACE3029205, BRACE3029447, BRACE3030538,
20 BRACE3031161, BRACE3031184, BRACE3031185, BRACE3031315,
BRACE3031372, BRACE3031579, BRACE3031728, BRACE3031743,
BRACE3031843, BRACE3032385, BRACE3032537, BRACE3032538,
BRACE3032631, BRACE3032980, BRACE3033525, BRACE3034183,
BRACE3034389, BRACE3034964, BRACE3034993, BRACE3035168,
25 BRACE3036156, BRACE3036271, BRACE3036283, BRACE3037612,
BRACE3037637, BRACE3037803, BRACE3038012, BRACE3038030,
BRACE3038570, BRACE3038760, BRACE3039288, BRACE3039358,
BRACE3039378, BRACE3039454, BRACE3040012, BRACE3040239,
BRACE3040504, BRACE3040644, BRACE3040863, BRACE3041059,
30 BRACE3041162, BRACE3041827, BRACE3042046, BRACE3042210,
BRACE3042326, BRACE3042409, BRACE3042432, BRACE3042594,
BRACE3043597, BRACE3044090, BRACE3044172, BRACE3044247,
BRACE3044377, BRACE3044495, BRACE3045078, BRACE3045145,
BRACE3045424, BRACE3045708, BRACE3045981, BRACE3046049,
35 BRACE3046152, BRACE3046294, BRACE3046466, BRACE3046491,
BRACE3046609, BRACE3046837, BRACE3046855, BRACE3046966,

BRACE3047018, BRACE3047482, BRACE3047801, BRAMY2031516,
BRAMY3002329, BRAMY3004126, BRAMY3004364, BRAMY3005912,
BRAMY3008436, BRAMY3009491, BRAWH2000256, BRAWH2002333,
BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796,
5 BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866,
BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223,
BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785,
BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638,
BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573,
10 BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037,
BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167,
BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461,
BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833,
BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577,
15 BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929,
BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009,
BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609,
BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610,
BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180,
20 BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980,
BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969,
BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820,
BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928,
BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641,
25 BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431,
BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719,
BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172,
BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231,
BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349,
30 BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533,
BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675,
BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223,
BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313,
BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772,
35 BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342,
BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571,

BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513,
BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668,
BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403,
BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077,
5 BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561,
BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533,
BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252,
BRAWH3038324, BRCAN2010665, BRCAN2019953, BRCAN2022126,
BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077,
10 BRHIP2029643, BRHIP3001360, BRHIP3001573, BRHIP3002000,
BRHIP3002114, BRHIP3003063, BRHIP3003126, BRHIP3003961,
BRHIP3003984, BRHIP3004215, BRHIP3004774, BRHIP3005801,
BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675,
BRHIP3017855, BRHIP3018784, BRHIP3021019, BRHIP3028246,
15 BRHIP3028570, BRSSN2011843, BRSSN2013696, BRSTN2010089,
BRSTN2011961, BRSTN2012069, BRSTN2016992, BRTHA2033155,
BRTHA2035743, BRTHA3003736, BRTHA3005988, BRTHA3009858,
BRTHA3010135, BRTHA3010212, BRTHA3010530, BRTHA3011194,
BRTHA3011265, BRTHA3011998, BRTHA3017791, BRTHA3020771,
20 BRTHA3021708, BRTHA3021971, BRTHA3023403, CHONS2002829,
CTONG2006235, CTONG2009033, CTONG2020582, CTONG2027959,
D9OST2003106, DFNES2001829, KIDNE2010049, KIDNE2017153,
LIVER2008465, MESAN2017133, NOVAR2000783, NT2RI2009233,
NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
25 NT2RP8001605, NT2RP8007920, NT2RP8009119, NTONG2008483,
NTONG2009468, OCBBF2003518, OCBBF2014745, OCBBF2018618,
OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240,
PROST2007444, TBAES2007428, TESTI2005112, TESTI2018867,
TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799,
30 TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005013,
TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908,
TESTI4022158, TESTI4029297, TESTI4032913, TESTI4043223,
THYMU3000776, THYMU3002887, THYMU3003350, THYMU3007308,
THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
35 THYMU3032798, THYMU3032867, THYMU3033626, THYMU3034671,
THYMU3037827, THYMU3038214, THYMU3044075, TLIVE2007736,

TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872,
 TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689,
 TRACH3007995, TRACH3008632, TRACH3009008, TRACH3010079,
 TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671,
 5 TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570,
 TRACH3036932, TRACH3038399, UTERU3000670, UTERU3010409,
 UTERU3013167, UTERU3015011
 BRACE3002184, BRACE3026993, BRACE3046450, BRAMY3008096,
 BRAWH3013197, BRAWH3028645, BRTHA3004432, TESTI4002988,
 10 TRACH1000193

These genes are involved in equilibrium sense or motor function.

Genes involved in signaling from sensory organs

15 The thalamus is an area which comprises many neurons
 strongly connected to the cerebrum, and which transmits sensory
 information from the spinal cord or such to the responsible area
 of the cerebrum. The thalamus also controls the direction of
 movement from the cerebrum. For example, the thalamus resolves
 20 vision into the elements of size, shape, and color, and resolves
 sound into volume and sweetness or harshness to the ear, and
 then transmits this information to the sensory area of the
 cerebral cortex. Thus, genes whose expression levels differ
 between tissues of the whole brain and the thalamus are expected
 25 to be involved in signaling from sensory organs. These genes
 can be used to elucidate the molecular mechanism underlying
 signaling controlled by the brain. cDNA libraries derived from
 the thalamus (BRTHA) and from whole tissues of a normal brain
 (BRAWH) were analyzed and compared (Table 8). Genes whose
 30 expression levels differed between the two were the 440 clones
 and eight clones listed below.

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE2002392,
 BRACE2012528, BRACE2019348, BRACE3004371, BRACE3004767,
 BRACE3019941, BRACE3022312, BRACE3022340, BRACE3031185,
 35 BRACE3031743, BRACE3032385, BRACE3032631, BRACE3036156,
 BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981,

BAMY2031516, BAMY3002329, BAMY3004126, BAMY3005912,
BAMY3008436, BAMY3009556, BAMY3010654, BAMY4001863,
BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364,
BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958,
5 BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053,
BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514,
BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884,
BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833,
BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335,
10 BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892,
BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867,
BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657,
BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331,
BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685,
15 BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662,
BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264,
BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017,
BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123,
BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260,
20 BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369,
BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529,
BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318,
BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574,
BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724,
25 BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542,
BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156,
BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421,
BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506,
BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420,
30 BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607,
BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880,
BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754,
BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538,
BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910,
35 BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298,
BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293,

BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114,
BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775,
BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914,
BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270,
5 BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394,
BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055,
BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2002892,
BRCAN2010665, BRCAN2020234, BRCAN2022126, BRCAN2025093,
BRCOC2006164, BRCOC2012386, BRHIP2013958, BRHIP2015153,
10 BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3002691,
BRHIP3002920, BRHIP3003063, BRHIP3003961, BRHIP3003984,
BRHIP3004215, BRHIP3004774, BRHIP3007223, BRHIP3007409,
BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784,
BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570,
15 BRSSN2015497, BRSTN2010089, BRSTN2011961, BRSTN2012069,
BRSTN2016992, BRTHA2000969, BRTHA2001304, BRTHA2001953,
BRTHA2002091, BRTHA2003759, BRTHA2005448, BRTHA2006720,
BRTHA2008502, BRTHA2008598, BRTHA2010672, BRTHA2012189,
BRTHA2014647, BRTHA2018304, BRTHA2019726, BRTHA2019743,
20 BRTHA2020400, BRTHA2020566, BRTHA2020642, BRTHA2020695,
BRTHA2020721, BRTHA2020781, BRTHA2020910, BRTHA2021212,
BRTHA2021440, BRTHA2021450, BRTHA2022074, BRTHA2022914,
BRTHA2022968, BRTHA2023402, BRTHA2023437, BRTHA2024177,
BRTHA2024354, BRTHA2024712, BRTHA2025869, BRTHA2026071,
25 BRTHA2026290, BRTHA2026311, BRTHA2027227, BRTHA2027229,
BRTHA2027250, BRTHA2028297, BRTHA2029969, BRTHA2030036,
BRTHA2030213, BRTHA2031517, BRTHA2031917, BRTHA2032763,
BRTHA2033122, BRTHA2033155, BRTHA2033320, BRTHA2033469,
BRTHA2033683, BRTHA2034281, BRTHA2034576, BRTHA2035743,
30 BRTHA2036055, BRTHA2036295, BRTHA2037247, BRTHA2038279,
BRTHA2038345, BRTHA2038353, BRTHA3000456, BRTHA3002411,
BRTHA3003225, BRTHA3003417, BRTHA3003736, BRTHA3005988,
BRTHA3006593, BRTHA3007469, BRTHA3007662, BRTHA3009858,
BRTHA3010135, BRTHA3010212, BRTHA3010469, BRTHA3010530,
35 BRTHA3010540, BRTHA3010717, BRTHA3011187, BRTHA3011194,
BRTHA3011229, BRTHA3011265, BRTHA3011306, BRTHA3011361,

BRTHA3011510, BRTHA3011892, BRTHA3011998, BRTHA3012265,
 BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3014105,
 BRTHA3014507, BRTHA3014547, BRTHA3014835, BRTHA3014854,
 BRTHA3014920, BRTHA3016616, BRTHA3017791, BRTHA3018409,
 5 BRTHA3018623, BRTHA3019183, BRTHA3020369, BRTHA3020771,
 BRTHA3021569, BRTHA3021708, BRTHA3021786, BRTHA3021971,
 BRTHA3022641, BRTHA3023403, BRTHA3023590, BRTHA3023929,
 BRTHA3024600, BRTHA3025073, BRTHA3026161, BRTHA3026180,
 BRTHA3026556, BRTHA3026916, BRTHA3027171, BRTHA3027318,
 10 BRTHA3027638, BRTHA3027820, BRTHA3027879, BRTHA3027957,
 BRTHA3028339, BRTHA3028505, CHONS2002829, CTONG2006235,
 CTONG2009033, CTONG2011801, CTONG2020582, D9OST2003106,
 DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133,
 NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
 15 NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920,
 NTONG2008483, OCBBF2003518, OCBBF2009536, OCBBF2018618,
 OCBBF3001333, OCBBF3004487, OCBBF3008835, PLACE6003004,
 PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292,
 TBAES2007428, TESTI2005112, TESTI2021654, TESTI2039342,
 20 TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602,
 TESTI4003703, TESTI4004210, TESTI4004695, TESTI4005399,
 TESTI4005653, TESTI4006441, TESTI4007965, TESTI4010979,
 TESTI4013474, TESTI4014908, TESTI4022158, TESTI4029297,
 TESTI4032913, THYMU3000776, THYMU3002887, THYMU3003350,
 25 THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350,
 THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214,
 THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037,
 TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,
 TRACH3007689, TRACH3008508, TRACH3008632, TRACH3009008,
 30 TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,
 TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
 UTERU3012414, UTERU3013167, UTERU3017995, UTERU3018172
 BRACE3046450, BRAWH3013197, BRAWH3028645, BRTHA3004432,
 35 BRTHA3024233, CTONG2002832, THYMU3046350, TRACH1000193

These genes are involved in signaling from sensory organs.

Genes involved in emotional reaction

The amygdala is the center of emotion in the brain. Information passing through the amygdala induces an emotional reaction, for example, panic or fear. When a strong fear reaction is produced due to the emotional evaluation of stimulus in the amygdala, the amygdala transmits an alert signal to each area of the brain. This results in various reactions such as sweating palms, palpitation, elevated blood pressure, and rapid secretion of adrenaline. In other words, the amygdala transmits signals which cause the body to be on the alert and is a tissue involved in a kind of defense instinct. Thus, genes whose expression levels differ between tissues of the whole brain and the amygdala are expected to be involved in emotional reaction. Such genes can be used to elucidate the molecular mechanism underlying emotional reaction, fear, or panic. cDNA libraries derived from the amygdala (BRAMY) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 9). Genes whose expression levels differed between the two were the 357 clones and nine clones listed below.

ASTRO2016114, BRACE2002392, BRACE2012528, BRACE2017397,
 BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340,
 BRACE3031185, BRACE3031315, BRACE3031743, BRACE3032385,
 BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432,
 BRACE3045981, BRAMY2015516, BRAMY2021098, BRAMY2022320,
 BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895,
 BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609,
 BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384,
 BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537,
 BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508,
 BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184,
 BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449,
 BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491,
 BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603,
 BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234,
 BRAMY4001652, BRAMY4001863, BRAMY4001913, BRAMY4002575,

BRAWMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078,
BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812,
BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,
BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305,
5 BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,
BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,
BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975,
BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886,
BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559,
10 BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602,
BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101,
BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005,
BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,
15 BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639,
BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825,
BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063,
BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
20 BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200,
BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012,
BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459,
BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
25 BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274,
BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242,
BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574,
BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
30 BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461,
BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385,
BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
35 BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743,

BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
 BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247,
 BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
 BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979,
 5 BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324,
 BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386,
 BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3002000,
 BRHIP3002691, BRHIP3003063, BRHIP3003984, BRHIP3004215,
 BRHIP3004774, BRHIP3005673, BRHIP3007223, BRHIP3007409,
 10 BRHIP3008320, BRHIP3012736, BRHIP3014675, BRHIP3017146,
 BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019,
 BRHIP3028246, BRHIP3028570, BRSTN2010089, BRSTN2012069,
 BRSTN2016992, BRTHA2026071, BRTHA2033155, BRTHA3003736,
 BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194,
 15 BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971,
 BRTHA3023403, BRTHA3026916, CHONS2002829, CTONG2006235,
 CTONG2009033, CTONG2020582, D9OST2003106, DFNES2001829,
 KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2010795,
 NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387,
 20 NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2000831,
 OCBBF2003518, OCBBF2018618, OCBBF2030927, OCBBF3001333,
 OCBBF3004487, OCBBF3009244, PLACE6008315, PLACE6010936,
 PLACE7004103, PLACE7006240, PROST2007444, SPLEN2012571,
 SYNOV4004210, SYNOV4009575, TBAES2007428, TESTI2005112,
 25 TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799,
 TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005399,
 TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158,
 TESTI4029297, TESTI4032913, TESTI4043223, TESTI4046073,
 THYMU3000776, THYMU3002887, THYMU3003350, THYMU3008105,
 30 THYMU3019476, THYMU3021586, THYMU3026000, THYMU3026306,
 THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827,
 THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752,
 TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717,
 TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008,
 35 TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342,
 TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855,

TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409,
UTERU3013167

BRACE3046450, BRAMY3008096, BRAWH3013197, BRAWH3028645,
BRTHA3004432, TESTI4002988, THYMU3046350, TRACH1000193,

5 TRACH3019290

These genes are involved in emotional reaction.

Cancer-related genes

10 Cancer tissues are assumed to express a distinct set of
genes distinct from normal tissues, and thus expression of these
genes can contribute to carcinogenesis in tissues and cells.
Thus, genes whose expression patterns in cancer tissues differ
from those in normal tissues are cancer-related genes. A search
was carried out for genes whose expression levels in cancer
15 tissues differed from those in normal tissues.

The result of comparative analysis of cDNA libraries
derived from breast tumor (TBAES) and normal breast (BEAST)
(Table 10) showed that the genes whose expression levels
differed between the two were ten and four clones as described
20 below.

BRSTN2011961, BRSTN2012069, TBAES2003917, TBAES2005361,
TBAES2007428, TBAES2007548, TBAES2007862, TESTI2005564,
TESTI4017854, TRACH3016805
TBAES2004105, TBAES2007379, TBAES2007481, TBAES2008133

25 The result of comparative analysis of cDNA libraries
derived from cervical tumor (TCERX) and normal cervical duct
(CERVX) (Table 11) showed that the genes whose expression levels
differed between the two were six clones as described below.

BRACE2017397, BRHIP2027077, BRSTN2011961, BRSTN2012069,
30 CERVX2000812, CERVX2000968

The result of comparative analysis of cDNA libraries
derived from colon tumor (TCOLN) and normal colon (COLON) (Table
12) showed that the genes whose expression levels were different
between the two were ten clones as described below.

BRSTN2011961, BRSTN2012069, COLON2001829, COLON2001866,
COLON2004351, COLON2004911, COLON2005623, COLON2005735,
OCBBF3001333, SMINT2017964

The result of comparative analysis of cDNA libraries
5 derived from esophageal tumor (TESOP) and normal esophagus
(NESOP) (Table 13) showed that the genes whose expression levels
were different between the two were 14 clones as described below.
BRAMY3004364, BRAWH3027533, BRHIP3007223, BRSTN2011961,
BRSTN2012069, CTONG2011801, CTONG3002518, SMINT2009292,
10 TESOP2002005, TESOP2003308, TESOP2004110, TESOP2008556,
UTERU3015011, UTERU3017995

The result of comparative analysis of cDNA libraries
derived from kidney tumor (TKIDN) and normal kidney (KIDNE)
(Table 14) showed that the genes whose expression levels were
15 different between the two were 43 clones as described below.
BRACE2002392, BRACE2012528, BRACE3004371, BRAMY2039630,
BRAMY3004364, BRAMY3008436, BRAWH2004078, BRAWH3012662,
BRAWH3021574, BRAWH3022651, BRAWH3037428, BRCAN2019953,
BRCAN2022126, BRHIP3002000, BRHIP3002691, BRHIP3012997,
20 BRHIP3020046, BRSTN2012069, BRSTN2016992, BRTHA3010212,
CTONG2006235, KIDNE2004531, KIDNE2010049, KIDNE2014496,
KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268,
NT2RI2015533, NT2RP7007387, OCBBF3004487, PLACE6008315,
SYNOV4004210, TESTI2005112, THYMU3001776, THYMU3002887,
25 THYMU3029795, THYMU3032867, TKIDN2000319, TKIDN2003396,
TKIDN2010602, TKIDN2011051, TKIDN2011160

The result of comparative analysis of cDNA libraries
derived from liver tumor (TLIVE) and normal liver (LIVER) (Table
15) showed that the genes whose expression levels were different
30 between the two were 14 and two clones as described below.
BRAWH3022651, BRCAN2020412, BRSTN2012069, BRTHA3003736,
CTONG2006235, LIVER2008465, TESTI4013474, THYMU3002887,
THYMU3038158, TLIVE2000142, TLIVE2001616, TLIVE2007736,
TLIVE2008797, TRACH3027229
35 THYMU3046350, TLIVE2007192

The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) (Table 16) showed that the genes whose expression levels were different between the two were 17 clones as described below.

5 BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069,
HLUNG2012600, MESAN2009156, NTONG2008483, PROST2007444,
TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297,
THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428,
TRACH3022198

10 The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table 17) showed the genes whose expression levels were different between the two were three clones as described below.
BRSTN2012069, NOVAR2000783, THYMU3002887

15 The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) (Table 18) showed that the genes whose expression levels were different between the two were 9 clones as described below.
BRSTN2012069, CHONS2002829, STOMA2003894, STOMA2004663,
20 THYMU3001776, TSTOM2000235, TSTOM2001571, TSTOM2002611,
TSTOM2002682

The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) (Table 19) showed that the genes whose expression levels were
25 different between the two were 128 and three clones as described below.

BRACE2012528, BRACE2017397, BRACE3004371, BRACE3036283,
BRACE3040863, BRAMY2031516, BRAMY3005184, BRAWH2004078,
BRAWH3004350, BRAWH3022651, BRAWH3024186, BRAWH3029806,
30 BRAWH3031342, BRCAN2022126, BRHIP3001076, BRHIP3002000,
BRHIP3002141, BRHIP3005307, BRHIP3007223, BRHIP3017855,
BRHIP3020046, BRSTN2010089, BRSTN2011961, BRSTN2012069,
BRSTN2016892, BRTHA3003736, BRTHA3011265, BRTHA3023403,
BRTHA3027879, CHONS2002829, CTONG2001932, CTONG2003517,
35 CTONG2006235, CTONG2011801, CTONG3002518, DFNES2001829,
KIDNE2010049, LIVER2008465, NT2RI3005923, OCBBF3001333,

OCBBF3004487, PLACE6008315, PLACE7006240, PROST2007444,
 SPLEN2012571, SYNOV4000598, SYNOV4009575, T1ESE2000904,
 TESTI4002072, TESTI4002195, TESTI4002774, TESTI4002799,
 TESTI4003703, TESTI4003944, TESTI4005399, TESTI4005653,
 5 TESTI4024245, TESTI4029297, THYMU3002887, THYMU3021586,
 THYMU3026350, THYMU3032798, THYMU3034616, THYMU3034671,
 TRACH3003872, TRACH3005699, TRACH3006800, TRACH3008632,
 TRACH3009008, TUTER1000014, TUTER2001433, UTERU2000300,
 UTERU2014998, UTERU2016464, UTERU2016669, UTERU2020226,
 10 UTERU2022955, UTERU2023941, UTERU2024042, UTERU2027369,
 UTERU2028377, UTERU2029660, UTERU2035926, UTERU2037423,
 UTERU3000670, UTERU3001029, UTERU3001394, UTERU3001946,
 UTERU3004635, UTERU3005264, UTERU3005422, UTERU3006538,
 UTERU3006720, UTERU3007108, UTERU3009775, UTERU3010029,
 15 UTERU3010409, UTERU3010604, UTERU3010892, UTERU3010919,
 UTERU3011092, UTERU3011398, UTERU3011558, UTERU3011579,
 UTERU3011837, UTERU3012293, UTERU3012414, UTERU3012476,
 UTERU3012599, UTERU3012999, UTERU3013167, UTERU3013302,
 UTERU3014274, UTERU3014647, UTERU3014906, UTERU3015011,
 20 UTERU3015299, UTERU3015647, UTERU3015844, UTERU3016070,
 UTERU3016273, UTERU3016274, UTERU3016308, UTERU3017441,
 UTERU3017626, UTERU3017995, UTERU3018172, UTERU3018255
 UTERU2017492, UTERU2025415, UTERU2036507

The result of comparative analysis of cDNA libraries
 25 derived from tongue cancer (CTONG) and normal tongue (NTONG)
 (Table 20) showed that the genes whose expression levels were
 different between the two were 67 and two clones as described
 below.

BRACE2012528, BRAMY4001863, BRAWH3021574, BRAWH3022651,
 30 BRAWH3024186, BRHIP2027077, BRHIP3001573, BRHIP3002000,
 BRHIP3007223, BRHIP3012997, BRHIP3020046, BRSSN2013696,
 BRSTN2011961, BRSTN2012069, BRTHA2027229, BRTHA2033155,
 BRTHA3011194, BRTHA3022641, CTONG2001932, CTONG2003517,
 CTONG2006235, CTONG2008989, CTONG2009033, CTONG2009570,
 35 CTONG2010330, CTONG2011801, CTONG2012123, CTONG2014206,
 CTONG2014959, CTONG2020582, CTONG2026987, CTONG2027150,

CTONG2027591, CTONG2027783, CTONG2027959, CTONG3001605,
 CTONG3002518, CTONG3002588, CTONG3003669, CTONG3008223,
 NT2RI2009233, NTONG2002278, NTONG2003805, NTONG2004829,
 NTONG2008483, NTONG2009468, OCBBF3004487, PLACE6008315,
 5 PLACE7004103, SKNMC2003639, SPLEN2012571, SPLEN2019092,
 SYNOV4009575, T1ESE2000904, TESTI2005564, TESTI2018867,
 TESTI4002799, TESTI4005653, TESTI4032913, THYMU3021586,
 THYMU3047115, TRACH3006717, TRACH3007625, TRACH3016805,
 TRACH3036932, TRACH3038399, UTERU2000300
 10 CTONG2002832, CTONG2003764

These genes are involved in cancer.

Further, there is a method to search for genes involved in
 development and differentiation, which is the expression
 frequency analysis in which the expression levels of genes are
 15 compared between developing and/or differentiating tissues
 and/or cells and adult tissues and/or cells. The genes involved
 in tissue development and/or differentiation are genes
 participating in tissue construction and expression of function,
 and thus are useful genes, which are available for regenerative
 20 medicine aiming at convenient regeneration of injured tissues.

By using the information of gene expression frequency
 gained from the database of nucleotide sequences of 1,402,069
 clones as described above, genes whose expression frequencies
 were different between developing and/or differentiating tissues
 25 and/or cells and adult tissues and/or cells were analyzed.

The result of comparative analysis of cDNA libraries
 derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain
 (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN
 or BRTHA) (Table 21) showed that the genes whose expression
 30 levels were different between the two were 916 and 13 clones as
 described below.

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE1000475,
 BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336,
 BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838,
 35 BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126,
 BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397,

BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992,
BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452,
BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956,
BRACE2030039, BRACE2032584, BRACE2033128, BRACE2034434,
5 BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607,
BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975,
BRACE3001403, BRACE3001973, BRACE3002344, BRACE3002541,
BRACE3002756, BRACE3003866, BRACE3004046, BRACE3004371,
BRACE3004767, BRACE3004887, BRACE3004981, BRACE3005870,
10 BRACE3005903, BRACE3006553, BRACE3007649, BRACE3007869,
BRACE3009075, BRACE3009265, BRACE3009392, BRACE3009416,
BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774,
BRACE3013418, BRACE3013874, BRACE3013986, BRACE3014523,
BRACE3014714, BRACE3015090, BRACE3015898, BRACE3016020,
15 BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810,
BRACE3016862, BRACE3017253, BRACE3018083, BRACE3019570,
BRACE3019611, BRACE3019817, BRACE3019941, BRACE3020356,
BRACE3020669, BRACE3021430, BRACE3021517, BRACE3021805,
BRACE3022051, BRACE3022303, BRACE3022312, BRACE3022340,
20 BRACE3022847, BRACE3023604, BRACE3024379, BRACE3024444,
BRACE3024497, BRACE3024537, BRACE3024879, BRACE3025627,
BRACE3025719, BRACE3026161, BRACE3026290, BRACE3026345,
BRACE3026456, BRACE3026802, BRACE3026844, BRACE3026947,
BRACE3027256, BRACE3027931, BRACE3028360, BRACE3028895,
25 BRACE3028998, BRACE3029005, BRACE3029021, BRACE3029205,
BRACE3029447, BRACE3030538, BRACE3031161, BRACE3031184,
BRACE3031185, BRACE3031315, BRACE3031372, BRACE3031579,
BRACE3031728, BRACE3031743, BRACE3031843, BRACE3032385,
BRACE3032537, BRACE3032538, BRACE3032631, BRACE3032980,
30 BRACE3033525, BRACE3034183, BRACE3034389, BRACE3034964,
BRACE3034993, BRACE3035168, BRACE3036156, BRACE3036271,
BRACE3036283, BRACE3037612, BRACE3037637, BRACE3037803,
BRACE3038012, BRACE3038030, BRACE3038570, BRACE3038760,
BRACE3039288, BRACE3039358, BRACE3039378, BRACE3039454,
35 BRACE3040012, BRACE3040239, BRACE3040504, BRACE3040644,
BRACE3040863, BRACE3041059, BRACE3041162, BRACE3041827,

BRACE3042046, BRACE3042210, BRACE3042326, BRACE3042409,
BRACE3042432, BRACE3042594, BRACE3043597, BRACE3044090,
BRACE3044172, BRACE3044247, BRACE3044377, BRACE3044495,
BRACE3045078, BRACE3045145, BRACE3045424, BRACE3045708,
5 BRACE3045981, BRACE3046049, BRACE3046152, BRACE3046294,
BRACE3046466, BRACE3046491, BRACE3046609, BRACE3046837,
BRACE3046855, BRACE3046966, BRACE3047018, BRACE3047482,
BRACE3047801, BRALZ2003119, BRALZ2007661, BRALZ2008930,
BRALZ2010842, BRALZ2011337, BRALZ2013621, BRALZ2013690,
10 BRALZ2014054, BRAMY2015516, BRAMY2021098, BRAMY2022320,
BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895,
BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609,
BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384,
BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537,
15 BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508,
BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184,
BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449,
BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491,
BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603,
20 BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234,
BRAMY4001652, BRAMY4001863, BRAMY4001913, BRAMY4002575,
BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078,
BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812,
BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,
25 BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305,
BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,
BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783,
BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975,
BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886,
30 BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559,
BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602,
BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101,
BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623,
BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005,
35 BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,
BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639,

BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825,
BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259,
BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063,
BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
5 BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200,
BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012,
BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643,
BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459,
BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
10 BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274,
BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242,
BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938,
BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574,
BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
15 BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461,
BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385,
BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810,
BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710,
BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
20 BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097,
BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743,
BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904,
BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247,
BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
25 BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979,
BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324,
BRCAN2000923, BRCAN2002662, BRCAN2002892, BRCAN2003269,
BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2007525,
BRCAN2008701, BRCAN2009168, BRCAN2010547, BRCAN2010581,
30 BRCAN2010665, BRCAN2015402, BRCAN2015757, BRCAN2018269,
BRCAN2018667, BRCAN2019653, BRCAN2019907, BRCAN2019953,
BRCAN2020234, BRCAN2020331, BRCAN2020412, BRCAN2020467,
BRCAN2020880, BRCAN2021325, BRCAN2021452, BRCAN2021718,
BRCAN2022126, BRCAN2025093, BRCAN2027593, BRCAN2028702,
35 BRCOC2001355, BRCOC2002777, BRCOC2006164, BRCOC2006639,
BRCOC2006942, BRCOC2009638, BRCOC2010115, BRCOC2012386,

BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177,
BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125,
BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735,
BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563,
5 BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626,
BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338,
BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878,
BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141,
BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931,
10 BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340,
BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845,
BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710,
BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037,
BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673,
15 BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294,
BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172,
BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409,
BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082,
BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753,
20 BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269,
BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185,
BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997,
BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675,
BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109,
25 BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855,
BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880,
BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733,
BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656,
BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795,
30 BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160,
BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246,
BRHIP3028570, BRHIP3028742, BRSSN2004303, BRSSN2004710,
BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198,
BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2000312,
35 BRSTN2006466, BRSTN2006638, BRSTN2008475, BRSTN2009247,
BRSTN2010089, BRSTN2010416, BRSTN2011688, BRSTN2011961,

BRSTN2012069, BRSTN2016892, BRSTN2016918, BRSTN2016992,
 BRSTN2017104, BRSTN2017151, BRSTN2018712, BRTHA2000969,
 BRTHA2001304, BRTHA2001953, BRTHA2002091, BRTHA2003759,
 BRTHA2005448, BRTHA2006720, BRTHA2008502, BRTHA2008598,
 5 BRTHA2010672, BRTHA2012189, BRTHA2014647, BRTHA2018304,
 BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566,
 BRTHA2020642, BRTHA2020695, BRTHA2020721, BRTHA2020781,
 BRTHA2020910, BRTHA2021212, BRTHA2021440, BRTHA2021450,
 BRTHA2022074, BRTHA2022914, BRTHA2022968, BRTHA2023402,
 10 BRTHA2023437, BRTHA2024177, BRTHA2024354, BRTHA2024712,
 BRTHA2025869, BRTHA2026071, BRTHA2026290, BRTHA2026311,
 BRTHA2027227, BRTHA2027229, BRTHA2027250, BRTHA2028297,
 BRTHA2029969, BRTHA2030036, BRTHA2030213, BRTHA2031517,
 BRTHA2031917, BRTHA2032763, BRTHA2033122, BRTHA2033155,
 15 BRTHA2033320, BRTHA2033469, BRTHA2033683, BRTHA2034281,
 BRTHA2034576, BRTHA2035743, BRTHA2036055, BRTHA2036295,
 BRTHA2037247, BRTHA2038279, BRTHA2038345, BRTHA2038353,
 BRTHA3000456, BRTHA3002411, BRTHA3003225, BRTHA3003417,
 BRTHA3003736, BRTHA3005988, BRTHA3006593, BRTHA3007469,
 20 BRTHA3007662, BRTHA3009858, BRTHA3010135, BRTHA3010212,
 BRTHA3010469, BRTHA3010530, BRTHA3010540, BRTHA3010717,
 BRTHA3011187, BRTHA3011194, BRTHA3011229, BRTHA3011265,
 BRTHA3011306, BRTHA3011361, BRTHA3011510, BRTHA3011892,
 BRTHA3011998, BRTHA3012265, BRTHA3013860, BRTHA3013882,
 25 BRTHA3014000, BRTHA3014105, BRTHA3014507, BRTHA3014547,
 BRTHA3014835, BRTHA3014854, BRTHA3014920, BRTHA3016616,
 BRTHA3017791, BRTHA3018409, BRTHA3018623, BRTHA3019183,
 BRTHA3020369, BRTHA3020771, BRTHA3021569, BRTHA3021708,
 BRTHA3021786, BRTHA3021971, BRTHA3022641, BRTHA3023403,
 30 BRTHA3023590, BRTHA3023929, BRTHA3024600, BRTHA3025073,
 BRTHA3026161, BRTHA3026180, BRTHA3026556, BRTHA3026916,
 BRTHA3027171, BRTHA3027318, BRTHA3027638, BRTHA3027820,
 BRTHA3027879, BRTHA3027957, BRTHA3028339, BRTHA3028505,
 CHONS2002829, CTONG2001932, CTONG2006235, CTONG2009033,
 35 CTONG2011801, CTONG2020582, CTONG2027959, D9OST2003106,
 DFNES2001829, FCBBF3001018, FCBBF3002188, FCBBF3005160,

FCBBF3012443, FCBBF3020030, FCBBF3021191, FCBBF3024911,
 FCBBF5000384, FEBRA2000805, FEBRA2002260, FEBRA2012625,
 FEBRA2013069, FEBRA2013570, FEBRA2017736, FEBRA2017811,
 FEBRA2023498, FEBRA2026582, FEBRA2026977, FEBRA2028222,
 5 FEBRA2028457, JCMLC2000273, KIDNE2010049, KIDNE2017153,
 LIVER2008465, MESAN2017133, NOVAR2000783, NT2NE2011107,
 NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
 NT2RI3009524, NT2RP7007387, NT2RP8001604, NT2RP8001605,
 NT2RP8007920, NT2RP8009119, NTONG2008483, NTONG2009468,
 10 OCBBF2000831, OCBBF2003518, OCBBF2004478, OCBBF2007039,
 OCBBF2009536, OCBBF2014745, OCBBF2016928, OCBBF2018229,
 OCBBF2018618, OCBBF2019761, OCBBF2024589, OCBBF2024779,
 OCBBF2025631, OCBBF2030927, OCBBF2036019, OCBBF3000743,
 OCBBF3000830, OCBBF3001076, OCBBF3001202, OCBBF3001333,
 15 OCBBF3001616, OCBBF3003745, OCBBF3004487, OCBBF3004908,
 OCBBF3005330, OCBBF3005843, OCBBF3006986, OCBBF3007078,
 OCBBF3007704, OCBBF3008392, OCBBF3008835, OCBBF3009244,
 PLACE5000492, PLACE6003004, PLACE6008315, PLACE6010936,
 PLACE7004103, PLACE7006240, PROST2007444, PROST2017910,
 20 SMINT2009292, SMINT2012179, SPLEN2012571, SYNOV4004210,
 SYNOV4009575, T1ESE2000609, T1ESE2000904, TBAES2007428,
 TESTI2005112, TESTI2005564, TESTI2009497, TESTI2018867,
 TESTI2021654, TESTI2039342, TESTI4001569, TESTI4002072,
 TESTI4002195, TESTI4002774, TESTI4002799, TESTI4003602,
 25 TESTI4003703, TESTI4003944, TESTI4004210, TESTI4004695,
 TESTI4005013, TESTI4005399, TESTI4005653, TESTI4006441,
 TESTI4007965, TESTI4010979, TESTI4012960, TESTI4013474,
 TESTI4014908, TESTI4020596, TESTI4022158, TESTI4029297,
 TESTI4032913, TESTI4035770, TESTI4043223, TESTI4046073,
 30 THYMU3000776, THYMU3002887, THYMU3003007, THYMU3003350,
 THYMU3007308, THYMU3008105, THYMU3019476, THYMU3021586,
 THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798,
 THYMU3032867, THYMU3033626, THYMU3034671, THYMU3037827,
 THYMU3038214, THYMU3041428, THYMU3044075, TKIDN2000319,
 35 TLIVE2007736, TRACH2013585, TRACH3002752, TRACH3003037,
 TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,

TRACH3007689, TRACH3007995, TRACH3008508, TRACH3008632,
 TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885,
 TRACH3021544, TRACH3022109, TRACH3022198, TRACH3024342,
 TRACH3024671, TRACH3025316, TRACH3026303, TRACH3026676,
 5 TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399,
 TSTOM2000235, UTERU2000300, UTERU2027369, UTERU3000670,
 UTERU3005422, UTERU3010409, UTERU3012414, UTERU3013167,
 UTERU3015011, UTERU3016273, UTERU3017995, UTERU3018172
 BRACE3002184, BRACE3026993, BRACE3046450, BRAMY3008096,
 10 BRAWH3013197, BRAWH3028645, BRTHA3004432, BRTHA3024233,
 CTONG2002832, TESTI4002988, THYMU3046350, TRACH1000193,
 TRACH3019290

The result of comparative analysis of cDNA libraries
 derived from fetal heart (FEHRT) and adult heart (HEART) (Table
 15 22) showed that the genes whose expression levels were different
 between the two were ten clones as described below.

BRACE2012528, BRACE3004371, BRCAN2003814, BRSTN2011961,
 BRSTN2012069, BRSTN2016992, HEART2002531, NTONG2008483,
 PROST2002078, T1ESE2000609

20 The result of comparative analysis of cDNA libraries
 derived from fetal kidney (FEKID) and adult kidney (KIDNE)
 (Table 23) showed that the genes whose expression levels were
 different between the two were 21 clones as described below.

BRACE3004371, BRAMY2039630, BRAMY3004364, BRAWH2004078,
 25 BRHIP3002000, BRSTN2011961, BRSTN2012069, BRTHA2027229,
 KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987,
 KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RP7007387,
 TESTI2005112, TESTI4002799, THYMU3001776, THYMU3029795,
 THYMU3032867

30 The result of comparative analysis of cDNA libraries
 derived from fetal lung (FELNG) and adult lung (HLUNG) (Table
 24) showed that the genes whose expression levels were different
 between the two were 18 clones as described below.

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069,
 35 HLUNG2012600, MESAN2009156, NTONG2008483, PROST2007444,
 TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297,

THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428,
THYMU3044188, TRACH3022198

These genes are involved in regeneration of tissues and/or cells.

5 A nucleotide sequence information-based analysis was
carried out to identify the genes whose expression frequencies
are higher or lower in CD34+ cell (cell expressing a
glycoprotein CD34) treated with the osteoclast differentiation
factor (Molecular Medicine 38. 642-648. (2001)) than in the
10 untreated CD34+ cell, which is the precursor cell of
monocyte/macrophage line. The result of comparative analysis
for the frequency between the two cDNA libraries prepared from
the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells
treated with the osteoclast differentiation factor (D30ST, D60ST
15 or D90ST) showed following genes whose expression levels were
different between the two.

Table 2

20	Clone ID	CD34C	D30ST	D60ST	D90ST
	BRAWH3018063	0.000	30.813	0.000	0.000
	BRHIP3020046	0.000	0.000	68.001	0.000
	BRSSN2013696	0.000	41.698	0.000	0.000
25	BRSTN2012069	2.383	0.442	0.000	0.128
	BRTHA2027229	0.000	0.000	61.446	0.000
	D90ST2003106	0.000	0.000	0.000	93.096
	D90ST2003989	0.000	0.000	0.000	100.000
	D90ST2004417	0.000	0.000	0.000	100.000
30	OCBBF2016928	0.000	31.972	0.000	0.000
	TEST14005653	0.000	0.000	0.000	6.704
	TEST14013474	43.396	0.000	0.000	0.000
	THYMU3032798	0.000	0.000	0.000	26.074

A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2.

5 The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed following genes whose expression levels were different between the two.

10

Table 3

	Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
15	BLADE2004849	0.000	0.000	0.000	26.862
	BRACE2003628	0.000	16.442	0.000	0.000
	BRACE2012528	0.000	1.143	0.862	0.000
	BRAMY2023939	0.000	0.000	11.107	22.151
	BRAMY2031516	0.000	17.802	0.000	0.000
20	BRAMY4002628	0.000	17.119	12.908	0.000
	BRAWH3010461	0.000	0.000	3.733	0.000
	BRAWH3017259	0.000	0.000	0.000	50.722
	BRAWH3018063	0.000	0.000	14.389	0.000
	BRAWH3022651	0.000	3.948	0.000	0.000
25	BRAWH3024186	0.000	0.000	18.135	0.000
	BRCAN2019653	0.000	15.031	0.000	0.000
	BRCAN2022126	0.000	0.000	8.824	0.000
	BRCOC2012386	0.000	27.482	20.721	0.000
	BRHIP3002000	0.000	3.615	0.000	0.000
30	BRHIP3007223	0.000	4.859	3.664	0.000
	BRHIP3021019	0.000	0.000	14.074	0.000
	BRSTN2011961	8.334	0.000	0.526	3.149
	BRSTN2012069	0.000	0.479	0.052	0.788
	BRTHA2033155	0.000	0.000	7.729	0.000
35	BRTHA3010212	0.000	13.315	0.000	0.000
	BRTHA3011194	0.000	0.000	0.000	12.809

	BRTHA3011265	0.000	20.563	0.000	0.000
	BRTHA3017791	0.000	5.698	0.000	0.000
	BRTHA3021971	55.855	0.000	0.000	0.000
	CHONS2002829	0.000	0.000	2.969	0.000
5	CTONG2006235	0.000	3.948	0.000	0.000
	FCBBF3012443	0.000	0.000	49.588	0.000
	FEBRA2026582	0.000	0.000	42.162	0.000
	LIVER2008465	0.000	15.950	0.000	0.000
	NT2NE2011107	0.000	0.000	0.000	43.585
10	NT2NE2016041	0.000	0.000	0.000	100.000
	NT2RI2004818	0.000	0.000	100.000	0.000
	NT2RI2009233	0.000	5.436	4.099	0.000
	NT2RI2010795	0.000	0.000	29.973	0.000
	NT2RI2015533	0.000	0.000	2.824	0.000
15	NT2RI2023671	0.000	0.000	100.000	0.000
	NT2RI2028537	0.000	0.000	100.000	0.000
	NT2RI3001573	0.000	0.000	100.000	0.000
	NT2RI3001967	0.000	0.000	100.000	0.000
	NT2RI3005861	0.000	0.000	100.000	0.000
20	NT2RI3005923	0.000	0.000	35.423	0.000
	NT2RI3007095	0.000	0.000	100.000	0.000
	NT2RI3008179	0.000	0.000	100.000	0.000
	NT2RI3009480	0.000	0.000	68.547	0.000
	NT2RI3009524	0.000	0.000	64.504	0.000
25	NT2RP7003439	0.000	100.000	0.000	0.000
	NT2RP7007387	0.000	9.894	3.730	0.000
	NT2RP7014178	0.000	100.000	0.000	0.000
	NT2RP7014778	0.000	100.000	0.000	0.000
	NT2RP7016508	0.000	100.000	0.000	0.000
30	NT2RP7017139	0.000	100.000	0.000	0.000
	NT2RP7019682	0.000	100.000	0.000	0.000
	NT2RP7020343	0.000	100.000	0.000	0.000
	NT2RP8000633	0.000	100.000	0.000	0.000
	NT2RP8001363	0.000	100.000	0.000	0.000
35	NT2RP8001407	0.000	100.000	0.000	0.000
	NT2RP8001584	0.000	100.000	0.000	0.000

	NT2RP8001604	0.000	33.445	25.218	0.000
	NT2RP8001605	0.000	70.676	0.000	0.000
	NT2RP8003490	0.000	100.000	0.000	0.000
	NT2RP8003657	0.000	100.000	0.000	0.000
5	NT2RP8003787	0.000	100.000	0.000	0.000
	NT2RP8005546	0.000	59.103	0.000	0.000
	NT2RP8006452	0.000	100.000	0.000	0.000
	NT2RP8006521	0.000	100.000	0.000	0.000
	NT2RP8007416	0.000	100.000	0.000	0.000
10	NT2RP8007503	0.000	100.000	0.000	0.000
	NT2RP8007920	0.000	9.535	0.000	0.000
	NT2RP8008057	0.000	68.270	0.000	0.000
	NT2RP8009119	0.000	11.123	0.000	0.000
	NT2RP8009248	0.000	100.000	0.000	0.000
15	NTONG2008483	0.000	0.000	4.356	0.000
	OCBBF2003518	0.000	0.000	1.873	0.000
	OCBBF3001333	0.000	7.743	5.839	0.000
	OCBBF3004908	0.000	23.051	17.381	0.000
	PLACE7004103	0.000	6.234	9.400	0.000
20	PROST2017910	0.000	25.185	0.000	0.000
	SMINT2009292	0.000	0.000	6.446	0.000
	SPLEN2012571	0.000	15.323	5.777	0.000
	T1ESE2000904	0.000	11.128	0.000	0.000
	TEST14002072	0.000	8.048	6.068	0.000
25	TEST14002774	0.000	0.000	7.456	0.000
	TEST14002799	0.000	4.258	1.605	0.000
	TEST14005653	0.000	1.198	7.228	1.802
	TEST14007965	0.000	0.000	32.797	0.000
	TEST14012960	0.000	71.770	0.000	0.000
30	TEST14018436	0.000	0.000	9.457	0.000
	THYMU3001776	0.000	7.637	0.000	0.000
	THYMU3002887	0.000	1.880	0.000	14.135
	THYMU3029795	0.000	0.000	19.335	0.000
	THYMU3041428	0.000	0.614	0.463	0.000
35	THYMU3047115	0.000	0.000	0.747	0.000
	TRACH3003872	0.000	13.230	0.000	0.000

	TRACH3004424	0.000	0.000	30.905	0.000
	TRACH3006717	0.000	0.000	6.668	0.000
	TRACH3007625	0.000	2.833	2.136	4.260
	TRACH3009008	0.000	11.807	0.000	0.000
5	TRACH3016805	0.000	10.851	0.000	0.000
	TRACH3016885	0.000	0.000	14.459	0.000
	TRACH3026303	0.000	27.016	0.000	0.000
	UTERU2016669	0.000	0.000	0.000	29.924

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The result of comparative analysis of cDNA libraries derived from the cerebral cortex of Alzheimer patients (BRALZ and BRASW), and from whole tissues of a normal brain (BRAWH) showed the following genes whose expression levels differed

15

Table 4

Clone ID	BRAWH	BRALZ	BRASW
ASTR02016114	14.497	0.000	0.000
BRACE2002392	0.000	18.684	0.000
BRACE2012528	3.794	1.714	0.000
BRACE3004371	11.270	0.000	0.000
25 BRACE3004767	58.488	0.000	0.000
BRACE3022340	58.488	0.000	0.000
BRACE3031185	58.488	0.000	0.000
BRACE3031743	5.455	0.000	0.000
BRACE3032385	13.674	0.000	0.000
30 BRACE3032631	12.612	0.000	0.000
BRACE3039358	41.331	0.000	0.000
BRACE3040863	17.888	0.000	0.000
BRACE3042432	58.488	0.000	0.000
BRACE3045981	26.434	0.000	0.000
35 BRALZ2003119	0.000	100.000	0.000
BRALZ2007661	0.000	100.000	0.000

	BRALZ2008930	0.000	100.000	0.000
	BRALZ2010842	0.000	100.000	0.000
	BRALZ2011337	0.000	100.000	0.000
	BRALZ2013621	0.000	100.000	0.000
5	BRALZ2013690	0.000	100.000	0.000
	BRALZ2014054	0.000	38.408	0.000
	BRAMY2031516	14.772	0.000	0.000
	BRAMY3002329	20.323	0.000	0.000
	BRAMY3004126	49.811	0.000	0.000
10	BRAMY3005912	21.416	0.000	0.000
	BRAMY3008436	5.603	5.061	0.000
	BRAWH2000256	100.000	0.000	0.000
	BRAWH2002333	100.000	0.000	0.000
	BRAWH2004078	10.539	0.000	0.000
15	BRAWH2010364	34.464	0.000	0.000
	BRAWH2010619	100.000	0.000	0.000
	BRAWH2011796	100.000	0.000	0.000
	BRAWH2011812	13.544	0.000	0.000
	BRAWH2011958	100.000	0.000	0.000
20	BRAWH2012054	100.000	0.000	0.000
	BRAWH2012866	8.503	0.000	0.000
	BRAWH2013955	100.000	0.000	0.000
	BRAWH2014053	23.222	0.000	0.000
	BRAWH2016209	8.306	0.000	0.000
25	BRAWH2016223	100.000	0.000	0.000
	BRAWH2016305	4.308	0.000	0.000
	BRAWH2016514	35.037	0.000	0.000
	BRAWH2016562	49.499	0.000	0.000
	BRAWH2016785	100.000	0.000	0.000
30	BRAWH3000446	100.000	0.000	0.000
	BRAWH3000884	100.000	0.000	0.000
	BRAWH3001053	100.000	0.000	0.000
	BRAWH3001638	100.000	0.000	0.000
	BRAWH3001783	100.000	0.000	0.000
35	BRAWH3001833	100.000	0.000	0.000
	BRAWH3003244	100.000	0.000	0.000

	BRAWH3003573	20.162	0.000	0.000
	BRAWH3003975	100.000	0.000	0.000
	BRAWH3004335	100.000	0.000	0.000
	BRAWH3004350	16.580	0.000	0.000
5	BRAWH3005037	100.000	0.000	0.000
	BRAWH3005886	100.000	0.000	0.000
	BRAWH3005892	100.000	0.000	0.000
	BRAWH3005896	100.000	0.000	0.000
	BRAWH3008167	100.000	0.000	0.000
10	BRAWH3008559	100.000	0.000	0.000
	BRAWH3008867	100.000	0.000	0.000
	BRAWH3009961	47.417	0.000	0.000
	BRAWH3010461	16.435	0.000	0.000
	BRAWH3010602	100.000	0.000	0.000
15	BRAWH3010657	100.000	0.000	0.000
	BRAWH3010726	100.000	0.000	0.000
	BRAWH3010833	100.000	0.000	0.000
	BRAWH3011101	100.000	0.000	0.000
	BRAWH3011331	100.000	0.000	0.000
20	BRAWH3011402	100.000	0.000	0.000
	BRAWH3011577	100.000	0.000	0.000
	BRAWH3011623	100.000	0.000	0.000
	BRAWH3011685	100.000	0.000	0.000
	BRAWH3011907	47.417	0.000	0.000
25	BRAWH3011929	100.000	0.000	0.000
	BRAWH3012005	100.000	0.000	0.000
	BRAWH3012662	33.972	0.000	0.000
	BRAWH3012779	100.000	0.000	0.000
	BRAWH3013009	100.000	0.000	0.000
30	BRAWH3013049	100.000	0.000	0.000
	BRAWH3013264	100.000	0.000	0.000
	BRAWH3013508	100.000	0.000	0.000
	BRAWH3014609	44.597	0.000	0.000
	BRAWH3014639	100.000	0.000	0.000
35	BRAWH3015017	100.000	0.000	0.000
	BRAWH3015175	100.000	0.000	0.000

	BRAWH3015610	100.000	0.000	0.000
	BRAWH3015825	100.000	0.000	0.000
	BRAWH3016123	100.000	0.000	0.000
	BRAWH3016715	100.000	0.000	0.000
5	BRAWH3017180	28.251	0.000	0.000
	BRAWH3017259	13.996	0.000	0.000
	BRAWH3017260	100.000	0.000	0.000
	BRAWH3017477	100.000	0.000	0.000
	BRAWH3017980	49.811	0.000	0.000
10	BRAWH3018063	15.836	0.000	0.000
	BRAWH3018369	100.000	0.000	0.000
	BRAWH3018548	100.000	0.000	0.000
	BRAWH3018969	100.000	0.000	0.000
	BRAWH3019026	100.000	0.000	0.000
15	BRAWH3019529	100.000	0.000	0.000
	BRAWH3019594	100.000	0.000	0.000
	BRAWH3019820	100.000	0.000	0.000
	BRAWH3020200	100.000	0.000	0.000
	BRAWH3020318	100.000	0.000	0.000
20	BRAWH3020884	100.000	0.000	0.000
	BRAWH3020928	49.499	0.000	0.000
	BRAWH3021012	100.000	0.000	0.000
	BRAWH3021574	9.400	0.000	0.000
	BRAWH3021580	100.000	0.000	0.000
25	BRAWH3021641	100.000	0.000	0.000
	BRAWH3021643	100.000	0.000	0.000
	BRAWH3021724	100.000	0.000	0.000
	BRAWH3022347	100.000	0.000	0.000
	BRAWH3022431	100.000	0.000	0.000
30	BRAWH3022459	100.000	0.000	0.000
	BRAWH3022542	100.000	0.000	0.000
	BRAWH3022651	9.828	5.919	0.000
	BRAWH3022719	100.000	0.000	0.000
	BRAWH3022900	100.000	0.000	0.000
35	BRAWH3023156	100.000	0.000	0.000
	BRAWH3023168	100.000	0.000	0.000

	BRAWH3023172	0.916	0.000	0.000
	BRAWH3023274	100.000	0.000	0.000
	BRAWH3023421	100.000	0.000	0.000
	BRAWH3024186	19.959	0.000	0.000
5	BRAWH3024231	100.000	0.000	0.000
	BRAWH3024242	31.843	0.000	0.000
	BRAWH3024506	100.000	0.000	0.000
	BRAWH3024989	2.369	0.000	0.000
	BRAWH3026349	100.000	0.000	0.000
10	BRAWH3026938	6.894	8.303	0.000
	BRAWH3027420	100.000	0.000	0.000
	BRAWH3027440	58.488	0.000	0.000
	BRAWH3027533	11.008	0.000	0.000
	BRAWH3027574	47.417	0.000	0.000
15	BRAWH3027607	100.000	0.000	0.000
	BRAWH3027616	100.000	0.000	0.000
	BRAWH3027675	100.000	0.000	0.000
	BRAWH3027806	100.000	0.000	0.000
	BRAWH3027880	100.000	0.000	0.000
20	BRAWH3028202	100.000	0.000	0.000
	BRAWH3028223	100.000	0.000	0.000
	BRAWH3028461	100.000	0.000	0.000
	BRAWH3028754	100.000	0.000	0.000
	BRAWH3028796	100.000	0.000	0.000
25	BRAWH3029313	100.000	0.000	0.000
	BRAWH3029385	35.187	0.000	0.000
	BRAWH3029538	100.000	0.000	0.000
	BRAWH3029806	26.735	0.000	0.000
	BRAWH3030772	100.000	0.000	0.000
30	BRAWH3030810	21.287	0.000	0.000
	BRAWH3030910	100.000	0.000	0.000
	BRAWH3031054	100.000	0.000	0.000
	BRAWH3031342	10.856	0.000	0.000
	BRAWH3031710	100.000	0.000	0.000
35	BRAWH3032298	100.000	0.000	0.000
	BRAWH3032340	100.000	0.000	0.000

	BRAWH3032571	100.000	0.000	0.000
	BRAWH3033117	100.000	0.000	0.000
	BRAWH3033293	100.000	0.000	0.000
	BRAWH3033448	100.000	0.000	0.000
5	BRAWH3033513	100.000	0.000	0.000
	BRAWH3034097	100.000	0.000	0.000
	BRAWH3034114	100.000	0.000	0.000
	BRAWH3034134	100.000	0.000	0.000
	BRAWH3034668	100.000	0.000	0.000
10	BRAWH3034743	16.662	0.000	0.000
	BRAWH3034775	100.000	0.000	0.000
	BRAWH3034890	100.000	0.000	0.000
	BRAWH3035403	35.337	0.000	0.000
	BRAWH3035904	100.000	0.000	0.000
15	BRAWH3035914	100.000	0.000	0.000
	BRAWH3035936	70.575	0.000	0.000
	BRAWH3036077	100.000	0.000	0.000
	BRAWH3036247	54.530	0.000	0.000
	BRAWH3036270	100.000	0.000	0.000
20	BRAWH3036334	6.241	0.000	0.000
	BRAWH3036561	100.000	0.000	0.000
	BRAWH3037265	44.597	0.000	0.000
	BRAWH3037394	100.000	0.000	0.000
	BRAWH3037428	5.877	0.000	0.000
25	BRAWH3037533	100.000	0.000	0.000
	BRAWH3037979	100.000	0.000	0.000
	BRAWH3038055	100.000	0.000	0.000
	BRAWH3038230	100.000	0.000	0.000
	BRAWH3038252	100.000	0.000	0.000
30	BRAWH3038324	100.000	0.000	0.000
	BRCAN2010665	19.610	0.000	0.000
	BRCAN2019653	0.000	22.535	0.000
	BRCAN2022126	4.855	0.000	0.000
	BRCAN2025093	21.732	0.000	0.000
35	BRCOC2012386	11.403	0.000	0.000
	BRHIP2015153	20.038	0.000	0.000

	BRHIP2027077	2.020	0.000	0.000
	BRHIP3001573	24.474	0.000	0.000
	BRHIP3002000	4.500	2.710	0.000
	BRHIP3003063	10.960	0.000	0.000
5	BRHIP3003984	27.477	0.000	0.000
	BRHIP3004774	39.520	0.000	0.000
	BRHIP3007223	2.016	0.000	0.000
	BRHIP3007409	31.957	0.000	0.000
	BRHIP3008320	23.349	0.000	0.000
10	BRHIP3014675	37.925	0.000	0.000
	BRHIP3017855	15.316	0.000	0.000
	BRHIP3018784	6.930	0.000	0.000
	BRHIP3021019	7.745	0.000	0.000
	BRHIP3028246	22.147	0.000	0.000
15	BRHIP3028570	31.957	0.000	0.000
	BRSTN2010089	6.598	0.000	0.000
	BRSTN2012069	0.047	0.718	7.145
	BRSTN2016992	1.476	40.898	0.000
	BRTHA2033155	4.253	0.000	0.000
20	BRTHA3003736	4.302	0.000	0.000
	BRTHA3005988	31.076	0.000	0.000
	BRTHA3010135	20.010	0.000	0.000
	BRTHA3010212	5.525	0.000	0.000
	BRTHA3011194	3.534	0.000	0.000
25	BRTHA3011265	25.596	0.000	0.000
	BRTHA3017791	11.821	4.271	0.000
	BRTHA3020771	31.957	0.000	0.000
	BRTHA3021971	1.941	0.000	0.000
	BRTHA3023403	14.857	0.000	0.000
30	CTONG2006235	9.828	5.919	0.000
	CTONG2009033	25.755	0.000	0.000
	CTONG2020582	9.594	0.000	0.000
	D90ST2003106	6.904	0.000	0.000
	DFNES2001829	9.228	0.000	0.000
35	KIDNE2010049	3.438	0.000	0.000
	MESAN2017133	17.548	31.703	0.000

	NT2R12009233	6.767	0.000	0.000
	NT2R12015533	6.216	5.616	0.000
	NT2R13005923	19.493	0.000	0.000
	NT2R13009524	35.496	0.000	0.000
5	NT2RP7007387	6.158	0.000	0.000
	NT2RP8001605	29.324	0.000	0.000
	NT2RP8007920	1.978	0.000	0.000
	NTONG2008483	2.397	0.000	0.000
	OCBBF2003518	2.062	0.000	0.000
10	OCBBF2018618	16.218	0.000	0.000
	OCBBF3001333	9.639	0.000	0.000
	OCBBF3004487	4.531	0.000	0.000
	PLACE7004103	3.880	0.000	0.000
	PLACE7006240	25.174	0.000	0.000
15	PROST2007444	4.374	0.000	0.000
	PROST2017910	0.000	37.758	0.000
	TBAES2007428	5.371	0.000	0.000
	TESTI2005112	19.455	0.000	0.000
	TESTI2021654	9.773	0.000	0.000
20	TESTI4002072	16.696	0.000	0.000
	TESTI4002774	4.103	0.000	0.000
	TESTI4002799	1.767	0.000	0.000
	TESTI4003602	25.967	0.000	0.000
	TESTI4004210	36.051	0.000	0.000
25	TESTI4005399	7.797	0.000	0.000
	TESTI4005653	1.989	0.000	0.000
	TESTI4006441	60.471	0.000	0.000
	TESTI4013474	0.000	3.733	0.000
	TESTI4014908	36.051	0.000	0.000
30	TESTI4022158	53.386	0.000	0.000
	THYMU3000776	15.604	0.000	0.000
	THYMU3002887	4.680	0.000	0.000
	THYMU3003350	54.530	0.000	0.000
	THYMU3021586	20.651	0.000	0.000
35	THYMU3026000	49.066	0.000	0.000
	THYMU3026306	46.281	0.000	0.000

	THYMU3026350	14.291	0.000	0.000
	THYMU3032798	9.668	0.000	0.000
	THYMU3032867	12.871	0.000	0.000
	THYMU3037827	54.530	0.000	0.000
5	THYMU3038214	39.314	0.000	0.000
	THYMU3041428	0.000	0.000	96.263
	THYMU3044075	37.925	0.000	0.000
	TRACH2013585	23.471	0.000	0.000
	TRACH3002752	10.215	0.000	0.000
10	TRACH3003037	64.100	0.000	0.000
	TRACH3003872	2.745	0.000	0.000
	TRACH3004424	17.006	0.000	0.000
	TRACH3006717	18.347	0.000	0.000
	TRACH3007625	1.175	0.000	0.000
15	TRACH3007689	47.167	0.000	0.000
	TRACH3008632	25.351	0.000	0.000
	TRACH3009008	24.495	0.000	0.000
	TRACH3010079	48.305	0.000	0.000
	TRACH3016805	4.502	0.000	0.000
20	TRACH3016885	3.978	0.000	0.000
	TRACH3024342	47.167	0.000	0.000
	TRACH3024671	47.167	0.000	0.000
	TRACH3026303	5.605	0.000	0.000
	TRACH3026676	11.631	0.000	0.000
25	TRACH3028855	22.309	0.000	0.000
	TRACH3032570	47.167	0.000	0.000
	TRACH3036932	14.659	0.000	0.000
	TRACH3038399	12.435	0.000	0.000
	UTERU3010409	3.461	0.000	0.000
30	UTERU3013167	45.606	0.000	0.000
	BRACE3046450	21.984	0.000	0.000
	BRAWH3013197	100.000	0.000	0.000
	BRAWH3028645	100.000	0.000	0.000
	BRTHA3004432	32.087	0.000	0.000
35	TRACH1000193	21.722	0.000	0.000

The result of comparative analysis of cDNA libraries derived from the substantia nigra (BRSSN), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 5

	Clone ID	BRAWH	BRSSN
10	ASTR02016114	14.497	0.000
	BRACE2012528	3.794	0.000
	BRACE2017844	0.000	38.254
	BRACE3004371	11.270	0.000
15	BRACE3004767	58.488	0.000
	BRACE3022340	58.488	0.000
	BRACE3025719	0.000	67.040
	BRACE3026802	0.000	63.610
	BRACE3031185	58.488	0.000
20	BRACE3031743	5.455	0.000
	BRACE3032385	13.674	0.000
	BRACE3032631	12.612	0.000
	BRACE3039358	41.331	0.000
	BRACE3040863	17.888	0.000
25	BRACE3042432	58.488	0.000
	BRACE3045981	26.434	0.000
	BRAMY2031516	14.772	0.000
	BRAMY3002329	20.323	0.000
	BRAMY3004126	49.811	0.000
30	BRAMY3005912	21.416	0.000
	BRAMY3008436	5.603	10.427
	BRAWH2000256	100.000	0.000
	BRAWH2002333	100.000	0.000
	BRAWH2004078	10.539	0.000
35	BRAWH2010364	34.464	0.000
	BRAWH2010619	100.000	0.000

	BRAWH2011796	100.000	0.000
	BRAWH2011812	13.544	0.000
	BRAWH2011958	100.000	0.000
	BRAWH2012054	100.000	0.000
5	BRAWH2012866	8.503	0.000
	BRAWH2013955	100.000	0.000
	BRAWH2014053	23.222	0.000
	BRAWH2016209	8.306	0.000
	BRAWH2016223	100.000	0.000
10	BRAWH2016305	4.308	0.000
	BRAWH2016514	35.037	0.000
	BRAWH2016562	49.499	0.000
	BRAWH2016785	100.000	0.000
	BRAWH3000446	100.000	0.000
15	BRAWH3000884	100.000	0.000
	BRAWH3001053	100.000	0.000
	BRAWH3001638	100.000	0.000
	BRAWH3001783	100.000	0.000
	BRAWH3001833	100.000	0.000
20	BRAWH3003244	100.000	0.000
	BRAWH3003573	20.162	0.000
	BRAWH3003975	100.000	0.000
	BRAWH3004335	100.000	0.000
	BRAWH3004350	16.580	0.000
25	BRAWH3005037	100.000	0.000
	BRAWH3005886	100.000	0.000
	BRAWH3005892	100.000	0.000
	BRAWH3005896	100.000	0.000
	BRAWH3008167	100.000	0.000
30	BRAWH3008559	100.000	0.000
	BRAWH3008867	100.000	0.000
	BRAWH3009961	47.417	0.000
	BRAWH3010461	16.435	7.646
	BRAWH3010602	100.000	0.000
35	BRAWH3010657	100.000	0.000
	BRAWH3010726	100.000	0.000

	BRAWH3010833	100.000	0.000
	BRAWH3011101	100.000	0.000
	BRAWH3011331	100.000	0.000
	BRAWH3011402	100.000	0.000
5	BRAWH3011577	100.000	0.000
	BRAWH3011623	100.000	0.000
	BRAWH3011685	100.000	0.000
	BRAWH3011907	47.417	0.000
	BRAWH3011929	100.000	0.000
10	BRAWH3012005	100.000	0.000
	BRAWH3012662	33.972	0.000
	BRAWH3012779	100.000	0.000
	BRAWH3013009	100.000	0.000
	BRAWH3013049	100.000	0.000
15	BRAWH3013264	100.000	0.000
	BRAWH3013508	100.000	0.000
	BRAWH3014609	44.597	0.000
	BRAWH3014639	100.000	0.000
	BRAWH3015017	100.000	0.000
20	BRAWH3015175	100.000	0.000
	BRAWH3015610	100.000	0.000
	BRAWH3015825	100.000	0.000
	BRAWH3016123	100.000	0.000
	BRAWH3016715	100.000	0.000
25	BRAWH3017180	28.251	0.000
	BRAWH3017259	13.996	0.000
	BRAWH3017260	100.000	0.000
	BRAWH3017477	100.000	0.000
	BRAWH3017980	49.811	0.000
30	BRAWH3018063	15.836	0.000
	BRAWH3018369	100.000	0.000
	BRAWH3018548	100.000	0.000
	BRAWH3018969	100.000	0.000
	BRAWH3019026	100.000	0.000
35	BRAWH3019529	100.000	0.000
	BRAWH3019594	100.000	0.000

	BRAWH3019820	100.000	0.000
	BRAWH3020200	100.000	0.000
	BRAWH3020318	100.000	0.000
	BRAWH3020884	100.000	0.000
5	BRAWH3020928	49.499	0.000
	BRAWH3021012	100.000	0.000
	BRAWH3021574	9.400	17.492
	BRAWH3021580	100.000	0.000
	BRAWH3021641	100.000	0.000
10	BRAWH3021643	100.000	0.000
	BRAWH3021724	100.000	0.000
	BRAWH3022347	100.000	0.000
	BRAWH3022431	100.000	0.000
	BRAWH3022459	100.000	0.000
15	BRAWH3022542	100.000	0.000
	BRAWH3022651	9.828	6.097
	BRAWH3022719	100.000	0.000
	BRAWH3022900	100.000	0.000
	BRAWH3023156	100.000	0.000
20	BRAWH3023168	100.000	0.000
	BRAWH3023172	0.916	0.000
	BRAWH3023274	100.000	0.000
	BRAWH3023421	100.000	0.000
	BRAWH3024186	19.959	0.000
25	BRAWH3024231	100.000	0.000
	BRAWH3024242	31.843	0.000
	BRAWH3024506	100.000	0.000
	BRAWH3024989	2.369	0.000
	BRAWH3026349	100.000	0.000
30	BRAWH3026938	6.894	0.000
	BRAWH3027420	100.000	0.000
	BRAWH3027440	58.488	0.000
	BRAWH3027533	11.008	0.000
	BRAWH3027574	47.417	0.000
35	BRAWH3027607	100.000	0.000
	BRAWH3027616	100.000	0.000

	BRAWH3027675	100.000	0.000
	BRAWH3027806	100.000	0.000
	BRAWH3027880	100.000	0.000
	BRAWH3028202	100.000	0.000
5	BRAWH3028223	100.000	0.000
	BRAWH3028461	100.000	0.000
	BRAWH3028754	100.000	0.000
	BRAWH3028796	100.000	0.000
	BRAWH3029313	100.000	0.000
10	BRAWH3029385	35.187	0.000
	BRAWH3029538	100.000	0.000
	BRAWH3029806	26.735	0.000
	BRAWH3030772	100.000	0.000
	BRAWH3030810	21.287	0.000
15	BRAWH3030910	100.000	0.000
	BRAWH3031054	100.000	0.000
	BRAWH3031342	10.856	0.000
	BRAWH3031710	100.000	0.000
	BRAWH3032298	100.000	0.000
20	BRAWH3032340	100.000	0.000
	BRAWH3032571	100.000	0.000
	BRAWH3033117	100.000	0.000
	BRAWH3033293	100.000	0.000
	BRAWH3033448	100.000	0.000
25	BRAWH3033513	100.000	0.000
	BRAWH3034097	100.000	0.000
	BRAWH3034114	100.000	0.000
	BRAWH3034134	100.000	0.000
	BRAWH3034668	100.000	0.000
30	BRAWH3034743	16.662	0.000
	BRAWH3034775	100.000	0.000
	BRAWH3034890	100.000	0.000
	BRAWH3035403	35.337	0.000
	BRAWH3035904	100.000	0.000
35	BRAWH3035914	100.000	0.000
	BRAWH3035936	70.575	0.000

	BRAWH3036077	100.000	0.000
	BRAWH3036247	54.530	0.000
	BRAWH3036270	100.000	0.000
	BRAWH3036334	6.241	0.000
5	BRAWH3036561	100.000	0.000
	BRAWH3037265	44.597	0.000
	BRAWH3037394	100.000	0.000
	BRAWH3037428	5.877	21.873
	BRAWH3037533	100.000	0.000
10	BRAWH3037979	100.000	0.000
	BRAWH3038055	100.000	0.000
	BRAWH3038230	100.000	0.000
	BRAWH3038252	100.000	0.000
	BRAWH3038324	100.000	0.000
15	BRCAN2010665	19.610	0.000
	BRCAN2022126	4.855	0.000
	BRCAN2025093	21.732	0.000
	BRCOC2012386	11.403	0.000
	BRHIP2015153	20.038	0.000
20	BRHIP2027077	2.020	0.000
	BRHIP2029643	0.000	55.599
	BRHIP3001573	24.474	0.000
	BRHIP3002000	4.500	5.583
	BRHIP3003063	10.960	0.000
25	BRHIP3003984	27.477	0.000
	BRHIP3004774	39.520	0.000
	BRHIP3007223	2.016	0.000
	BRHIP3007409	31.957	0.000
	BRHIP3008320	23.349	0.000
30	BRHIP3014675	37.925	0.000
	BRHIP3017855	15.316	0.000
	BRHIP3018784	6.930	0.000
	BRHIP3020046	0.000	3.770
	BRHIP3021019	7.745	0.000
35	BRHIP3028246	22.147	0.000
	BRHIP3028570	31.957	0.000

	BRSSN2004303	0.000	100.000
	BRSSN2004710	0.000	100.000
	BRSSN2008464	0.000	100.000
	BRSSN2011843	0.000	44.546
5	BRSSN2012157	0.000	100.000
	BRSSN2012198	0.000	100.000
	BRSSN2013696	0.000	13.293
	BRSSN2015497	0.000	26.619
	BRSSN2018218	0.000	100.000
10	BRSTN2010089	6.598	0.000
	BRSTN2011961	0.000	1.078
	BRSTN2012069	0.047	0.000
	BRSTN2016992	1.476	5.495
	BRSTN2017104	0.000	7.257
15	BRTHA2033155	4.253	15.830
	BRTHA3003736	4.302	0.000
	BRTHA3005988	31.076	0.000
	BRTHA3010135	20.010	0.000
	BRTHA3010212	5.525	0.000
20	BRTHA3011194	3.534	0.000
	BRTHA3011265	25.596	0.000
	BRTHA3017791	11.821	0.000
	BRTHA3020771	31.957	0.000
	BRTHA3021971	1.941	0.000
25	BRTHA3023403	14.857	0.000
	CTONG2006235	9.828	6.097
	CTONG2009033	25.755	0.000
	CTONG2011801	0.000	11.021
	CTONG2020582	9.594	0.000
30	D90ST2003106	6.904	0.000
	DFNES2001829	9.228	0.000
	KIDNE2010049	3.438	0.000
	MESAN2017133	17.548	0.000
	NT2RI2009233	6.767	0.000
35	NT2RI2015533	6.216	0.000
	NT2RI3005923	19.493	0.000

	NT2RI3009524	35.496	0.000
	NT2RP7007387	6.158	0.000
	NT2RP8001605	29.324	0.000
	NT2RP8007920	1.978	7.363
5	NTONG2008483	2.397	0.000
	OCBBF2003518	2.062	0.000
	OCBBF2018618	16.218	0.000
	OCBBF3001333	9.639	0.000
	OCBBF3004487	4.531	0.000
10	PLACE7004103	3.880	0.000
	PLACE7006240	25.174	0.000
	PROST2007444	4.374	8.140
	SMINT2009292	0.000	13.202
	T1ESE2000904	0.000	8.593
15	TBAES2007428	5.371	0.000
	TESTI2005112	19.455	0.000
	TESTI2021654	9.773	0.000
	TESTI4002072	16.696	0.000
	TESTI4002774	4.103	0.000
20	TESTI4002799	1.767	0.000
	TESTI4003602	25.967	0.000
	TESTI4004210	36.051	0.000
	TESTI4005399	7.797	0.000
	TESTI4005653	1.989	0.000
25	TESTI4006441	60.471	0.000
	TESTI4014908	36.051	0.000
	TESTI4022158	53.386	0.000
	THYMU3000776	15.604	0.000
	THYMU3002887	4.680	2.903
30	THYMU3003350	54.530	0.000
	THYMU3021586	20.651	0.000
	THYMU3026000	49.066	0.000
	THYMU3026306	46.281	0.000
	THYMU3026350	14.291	0.000
35	THYMU3032798	9.668	0.000
	THYMU3032867	12.871	0.000

	THYMU3037827	54.530	0.000
	THYMU3038214	39.314	0.000
	THYMU3044075	37.925	0.000
	TRACH2013585	23.471	0.000
5	TRACH3002752	10.215	19.010
	TRACH3003037	64.100	0.000
	TRACH3003872	2.745	10.216
	TRACH3004424	17.006	0.000
	TRACH3006717	18.347	0.000
10	TRACH3007625	1.175	0.000
	TRACH3007689	47.167	0.000
	TRACH3008632	25.351	0.000
	TRACH3009008	24.495	0.000
	TRACH3010079	48.305	0.000
15	TRACH3016805	4.502	0.000
	TRACH3016885	3.978	0.000
	TRACH3022198	0.000	30.935
	TRACH3024342	47.167	0.000
	TRACH3024671	47.167	0.000
20	TRACH3026303	5.605	0.000
	TRACH3026676	11.631	0.000
	TRACH3028855	22.309	0.000
	TRACH3032570	47.167	0.000
	TRACH3036932	14.659	0.000
25	TRACH3038399	12.435	0.000
	UTERU3010409	3.461	0.000
	UTERU3013167	45.606	0.000
	BRACE3046450	21.984	0.000
	BRAWH3013197	100.000	0.000
30	BRAWH3028645	100.000	0.000
	BRTHA3004432	32.087	0.000
	TRACH1000193	21.722	0.000

35 The result of comparative analysis of cDNA libraries derived from the hippocampus (BRHIP), and from whole tissues of

a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 6

5			
	Clone ID	BRAWH	BRHIP
	ASTR02016114	14.497	0.000
	BRACE2002392	0.000	5.275
10	BRACE2012528	3.794	4.354
	BRACE2017359	0.000	41.817
	BRACE2017397	0.000	4.813
	BRACE2017844	0.000	5.243
	BRACE3004046	0.000	58.973
15	BRACE3004371	11.270	7.666
	BRACE3004767	58.488	0.000
	BRACE3009416	0.000	29.118
	BRACE3022340	58.488	0.000
	BRACE3027931	0.000	34.325
20	BRACE3029021	0.000	74.193
	BRACE3031185	58.488	0.000
	BRACE3031743	5.455	5.566
	BRACE3032385	13.674	20.927
	BRACE3032631	12.612	0.000
25	BRACE3036156	0.000	44.660
	BRACE3039358	41.331	21.084
	BRACE3040863	17.888	18.250
	BRACE3042326	0.000	35.796
	BRACE3042432	58.488	0.000
30	BRACE3045078	0.000	41.817
	BRACE3045981	26.434	0.000
	BRAMY2031516	14.772	7.536
	BRAMY3002329	20.323	34.558
	BRAMY3004126	49.811	0.000
35	BRAMY3005184	0.000	22.861
	BRAMY3005912	21.416	0.000

	B Ramsey3007078	0.000	50.312
	B Ramsey3008436	5.603	27.152
	B Ramsey4000915	0.000	50.312
	B BAWH2000256	100.000	0.000
5	B BAWH2002333	100.000	0.000
	B BAWH2004078	10.539	0.000
	B BAWH2010364	34.464	17.581
	B BAWH2010619	100.000	0.000
	B BAWH2011796	100.000	0.000
10	B BAWH2011812	13.544	0.000
	B BAWH2011958	100.000	0.000
	B BAWH2012054	100.000	0.000
	B BAWH2012866	8.503	4.337
	B BAWH2013955	100.000	0.000
15	B BAWH2014053	23.222	0.000
	B BAWH2016209	8.306	0.000
	B BAWH2016223	100.000	0.000
	B BAWH2016305	4.308	0.000
	B BAWH2016514	35.037	35.747
20	B BAWH2016562	49.499	50.501
	B BAWH2016785	100.000	0.000
	B BAWH3000446	100.000	0.000
	B BAWH3000884	100.000	0.000
	B BAWH3001053	100.000	0.000
25	B BAWH3001638	100.000	0.000
	B BAWH3001783	100.000	0.000
	B BAWH3001833	100.000	0.000
	B BAWH3003244	100.000	0.000
	B BAWH3003573	20.162	0.000
30	B BAWH3003975	100.000	0.000
	B BAWH3004335	100.000	0.000
	B BAWH3004350	16.580	0.000
	B BAWH3005037	100.000	0.000
	B BAWH3005886	100.000	0.000
35	B BAWH3005892	100.000	0.000
	B BAWH3005896	100.000	0.000

	BRAWH3008167	100.000	0.000
	BRAWH3008559	100.000	0.000
	BRAWH3008867	100.000	0.000
	BRAWH3009961	47.417	0.000
5	BRAWH3010461	16.435	8.384
	BRAWH3010602	100.000	0.000
	BRAWH3010657	100.000	0.000
	BRAWH3010726	100.000	0.000
	BRAWH3010833	100.000	0.000
10	BRAWH3011101	100.000	0.000
	BRAWH3011331	100.000	0.000
	BRAWH3011402	100.000	0.000
	BRAWH3011577	100.000	0.000
	BRAWH3011623	100.000	0.000
15	BRAWH3011685	100.000	0.000
	BRAWH3011907	47.417	0.000
	BRAWH3011929	100.000	0.000
	BRAWH3012005	100.000	0.000
	BRAWH3012662	33.972	11.553
20	BRAWH3012779	100.000	0.000
	BRAWH3013009	100.000	0.000
	BRAWH3013049	100.000	0.000
	BRAWH3013264	100.000	0.000
	BRAWH3013508	100.000	0.000
25	BRAWH3014609	44.597	0.000
	BRAWH3014639	100.000	0.000
	BRAWH3015017	100.000	0.000
	BRAWH3015175	100.000	0.000
	BRAWH3015610	100.000	0.000
30	BRAWH3015825	100.000	0.000
	BRAWH3016123	100.000	0.000
	BRAWH3016715	100.000	0.000
	BRAWH3017180	28.251	0.000
	BRAWH3017259	13.996	0.000
35	BRAWH3017260	100.000	0.000
	BRAWH3017477	100.000	0.000

	BRAWH3017980	49.811	0.000
	BRAWH3018063	15.836	0.000
	BRAWH3018369	100.000	0.000
	BRAWH3018548	100.000	0.000
5	BRAWH3018969	100.000	0.000
	BRAWH3019026	100.000	0.000
	BRAWH3019529	100.000	0.000
	BRAWH3019594	100.000	0.000
	BRAWH3019820	100.000	0.000
10	BRAWH3020200	100.000	0.000
	BRAWH3020318	100.000	0.000
	BRAWH3020884	100.000	0.000
	BRAWH3020928	49.499	50.501
	BRAWH3021012	100.000	0.000
15	BRAWH3021574	9.400	0.000
	BRAWH3021580	100.000	0.000
	BRAWH3021641	100.000	0.000
	BRAWH3021643	100.000	0.000
	BRAWH3021724	100.000	0.000
20	BRAWH3022347	100.000	0.000
	BRAWH3022431	100.000	0.000
	BRAWH3022459	100.000	0.000
	BRAWH3022542	100.000	0.000
	BRAWH3022651	9.828	5.014
25	BRAWH3022719	100.000	0.000
	BRAWH3022900	100.000	0.000
	BRAWH3023156	100.000	0.000
	BRAWH3023168	100.000	0.000
	BRAWH3023172	0.916	1.869
30	BRAWH3023274	100.000	0.000
	BRAWH3023421	100.000	0.000
	BRAWH3024186	19.959	10.182
	BRAWH3024231	100.000	0.000
	BRAWH3024242	31.843	32.488
35	BRAWH3024506	100.000	0.000
	BRAWH3024989	2.369	4.834

	BRAWH3026349	100.000	0.000
	BRAWH3026938	6.894	2.344
	BRAWH3027420	100.000	0.000
	BRAWH3027440	58.488	0.000
5	BRAWH3027533	11.008	0.000
	BRAWH3027574	47.417	0.000
	BRAWH3027607	100.000	0.000
	BRAWH3027616	100.000	0.000
	BRAWH3027675	100.000	0.000
10	BRAWH3027806	100.000	0.000
	BRAWH3027880	100.000	0.000
	BRAWH3028202	100.000	0.000
	BRAWH3028223	100.000	0.000
	BRAWH3028461	100.000	0.000
15	BRAWH3028754	100.000	0.000
	BRAWH3028796	100.000	0.000
	BRAWH3029313	100.000	0.000
	BRAWH3029385	35.187	17.949
	BRAWH3029538	100.000	0.000
20	BRAWH3029806	26.735	0.000
	BRAWH3030772	100.000	0.000
	BRAWH3030810	21.287	0.000
	BRAWH3030910	100.000	0.000
	BRAWH3031054	100.000	0.000
25	BRAWH3031342	10.856	0.000
	BRAWH3031710	100.000	0.000
	BRAWH3032298	100.000	0.000
	BRAWH3032340	100.000	0.000
	BRAWH3032571	100.000	0.000
30	BRAWH3033117	100.000	0.000
	BRAWH3033293	100.000	0.000
	BRAWH3033448	100.000	0.000
	BRAWH3033513	100.000	0.000
	BRAWH3034097	100.000	0.000
35	BRAWH3034114	100.000	0.000
	BRAWH3034134	100.000	0.000

	BRAWH3034668	100.000	0.000
	BRAWH3034743	16.662	21.249
	BRAWH3034775	100.000	0.000
	BRAWH3034890	100.000	0.000
5	BRAWH3035403	35.337	0.000
	BRAWH3035904	100.000	0.000
	BRAWH3035914	100.000	0.000
	BRAWH3035936	70.575	0.000
	BRAWH3036077	100.000	0.000
10	BRAWH3036247	54.530	0.000
	BRAWH3036270	100.000	0.000
	BRAWH3036334	6.241	19.102
	BRAWH3036561	100.000	0.000
	BRAWH3037265	44.597	0.000
15	BRAWH3037394	100.000	0.000
	BRAWH3037428	5.877	0.000
	BRAWH3037533	100.000	0.000
	BRAWH3037979	100.000	0.000
	BRAWH3038055	100.000	0.000
20	BRAWH3038230	100.000	0.000
	BRAWH3038252	100.000	0.000
	BRAWH3038324	100.000	0.000
	BRCAN2010665	19.610	13.338
	BRCAN2019953	0.000	9.704
25	BRCAN2022126	4.855	4.954
	BRCAN2025093	21.732	0.000
	BRCOC2012386	11.403	0.000
	BRHIP2006819	0.000	100.000
	BRHIP2006921	0.000	100.000
30	BRHIP2008756	0.000	100.000
	BRHIP2009177	0.000	100.000
	BRHIP2011199	0.000	55.026
	BRHIP2013958	0.000	36.661
	BRHIP2015153	20.038	20.443
35	BRHIP2016125	0.000	100.000
	BRHIP2017714	0.000	100.000

	BRHIP2020930	0.000	100.000
	BRHIP2021929	0.000	100.000
	BRHIP2023735	0.000	100.000
	BRHIP2024941	0.000	100.000
5	BRHIP2026346	0.000	100.000
	BRHIP2027077	2.020	2.061
	BRHIP2027563	0.000	100.000
	BRHIP2029529	0.000	100.000
	BRHIP2029643	0.000	15.240
10	BRHIP2029663	0.000	45.093
	BRHIP3000626	0.000	100.000
	BRHIP3000859	0.000	100.000
	BRHIP3001076	0.000	46.104
	BRHIP3001141	0.000	100.000
15	BRHIP3001338	0.000	100.000
	BRHIP3001360	0.000	58.973
	BRHIP3001481	0.000	38.435
	BRHIP3001573	24.474	24.970
	BRHIP3001878	0.000	100.000
20	BRHIP3002000	4.500	3.826
	BRHIP3002114	0.000	39.793
	BRHIP3002124	0.000	100.000
	BRHIP3002141	0.000	16.008
	BRHIP3002363	0.000	100.000
25	BRHIP3002691	0.000	16.923
	BRHIP3002920	0.000	64.789
	BRHIP3002931	0.000	100.000
	BRHIP3003063	10.960	55.910
	BRHIP3003126	0.000	74.193
30	BRHIP3003306	0.000	60.949
	BRHIP3003340	0.000	100.000
	BRHIP3003395	0.000	100.000
	BRHIP3003688	0.000	100.000
	BRHIP3003795	0.000	45.093
35	BRHIP3003845	0.000	10.774
	BRHIP3003961	0.000	19.351

	BRHIP3003984	27.477	28.033
	BRHIP3004215	0.000	13.851
	BRHIP3004710	0.000	100.000
	BRHIP3004725	0.000	100.000
5	BRHIP3004774	39.520	60.480
	BRHIP3004786	0.000	100.000
	BRHIP3005037	0.000	82.401
	BRHIP3005142	0.000	60.949
	BRHIP3005231	0.000	100.000
10	BRHIP3005307	0.000	46.104
	BRHIP3005673	0.000	52.564
	BRHIP3005801	0.000	19.121
	BRHIP3005944	0.000	100.000
	BRHIP3006279	0.000	100.000
15	BRHIP3006294	0.000	40.683
	BRHIP3006449	0.000	100.000
	BRHIP3006786	0.000	100.000
	BRHIP3006950	0.000	100.000
	BRHIP3007172	0.000	100.000
20	BRHIP3007195	0.000	75.737
	BRHIP3007223	2.016	2.057
	BRHIP3007291	0.000	100.000
	BRHIP3007409	31.957	32.604
	BRHIP3007424	0.000	100.000
25	BRHIP3007609	0.000	100.000
	BRHIP3007960	0.000	100.000
	BRHIP3008082	0.000	45.093
	BRHIP3008320	23.349	47.644
	BRHIP3008714	0.000	100.000
30	BRHIP3009672	0.000	100.000
	BRHIP3009753	0.000	1.187
	BRHIP3010289	0.000	100.000
	BRHIP3010916	0.000	45.093
	BRHIP3011082	0.000	100.000
35	BRHIP3011269	0.000	100.000
	BRHIP3011460	0.000	100.000

	BRHIP3011567	0.000	100.000
	BRHIP3011831	0.000	100.000
	BRHIP3012185	0.000	100.000
	BRHIP3012289	0.000	100.000
5	BRHIP3012357	0.000	100.000
	BRHIP3012736	0.000	33.611
	BRHIP3012997	0.000	2.837
	BRHIP3013078	0.000	100.000
	BRHIP3013588	0.000	60.949
10	BRHIP3013698	0.000	100.000
	BRHIP3014675	37.925	19.346
	BRHIP3015854	0.000	100.000
	BRHIP3016032	0.000	100.000
	BRHIP3016421	0.000	100.000
15	BRHIP3017109	0.000	100.000
	BRHIP3017146	0.000	66.943
	BRHIP3017256	0.000	100.000
	BRHIP3017558	0.000	100.000
	BRHIP3017855	15.316	11.720
20	BRHIP3018784	6.930	3.535
	BRHIP3019643	0.000	100.000
	BRHIP3019824	0.000	100.000
	BRHIP3019880	0.000	100.000
	BRHIP3019956	0.000	100.000
25	BRHIP3020046	0.000	2.067
	BRHIP3020155	0.000	100.000
	BRHIP3020733	0.000	55.026
	BRHIP3021019	7.745	7.901
	BRHIP3021499	0.000	100.000
30	BRHIP3021987	0.000	36.438
	BRHIP3022656	0.000	100.000
	BRHIP3023922	0.000	100.000
	BRHIP3024703	0.000	100.000
	BRHIP3024820	0.000	100.000
35	BRHIP3025795	0.000	100.000
	BRHIP3025844	0.000	100.000

	BRHIP3026231	0.000	100.000
	BRHIP3026651	0.000	100.000
	BRHIP3027160	0.000	100.000
	BRHIP3027191	0.000	100.000
5	BRHIP3027651	0.000	100.000
	BRHIP3027947	0.000	100.000
	BRHIP3028246	22.147	22.595
	BRHIP3028570	31.957	32.604
	BRHIP3028742	0.000	100.000
10	BRSTN2010089	6.598	0.000
	BRSTN2012069	0.047	0.000
	BRSTN2016992	1.476	2.510
	BRTHA2001953	0.000	9.766
	BRTHA2008502	0.000	22.073
15	BRTHA2031517	0.000	47.917
	BRTHA2033155	4.253	0.000
	BRTHA2035743	0.000	34.617
	BRTHA3003417	0.000	31.398
	BRTHA3003736	4.302	6.584
20	BRTHA3005988	31.076	0.000
	BRTHA3007662	0.000	64.789
	BRTHA3010135	20.010	0.000
	BRTHA3010212	5.525	0.000
	BRTHA3011194	3.534	10.818
25	BRTHA3011265	25.596	0.000
	BRTHA3012265	0.000	64.789
	BRTHA3017791	11.821	4.824
	BRTHA3020771	31.957	32.604
	BRTHA3021971	1.941	1.980
30	BRTHA3023403	14.857	15.157
	CHONS2002829	0.000	11.668
	CTONG2006235	9.828	5.014
	CTONG2009033	25.755	26.276
	CTONG2020582	9.594	1.958
35	D90ST2003106	6.904	0.000
	DFNES2001829	9.228	18.830

	KIDNE2010049	3.438	0.000
	LIVER2008465	0.000	6.752
	MESAN2017133	17.548	0.000
	NT2RI2009233	6.767	0.000
5	NT2RI2010795	0.000	16.827
	NT2RI2015533	6.216	1.586
	NT2RI3005923	19.493	0.000
	NT2RI3009524	35.496	0.000
	NT2RP7007387	6.158	2.094
10	NT2RP8001605	29.324	0.000
	NT2RP8007920	1.978	0.000
	NTONG2008483	2.397	0.815
	OCBBF2000831	0.000	9.824
	OCBBF2003518	2.062	0.000
15	OCBBF2018618	16.218	16.546
	OCBBF3001333	9.639	0.000
	OCBBF3004487	4.531	4.622
	PLACE7004103	3.880	5.278
	PLACE7006240	25.174	0.000
20	PROST2007444	4.374	5.578
	SMINT2012179	0.000	18.954
	SYNOV4004210	0.000	1.927
	TBAES2007428	5.371	0.000
	TESTI2005112	19.455	0.000
25	TESTI2005564	0.000	3.736
	TESTI2021654	9.773	0.000
	TESTI4001569	0.000	43.832
	TESTI4002072	16.696	20.440
	TESTI4002774	4.103	4.186
30	TESTI4002799	1.767	2.703
	TESTI4003602	25.967	0.000
	TESTI4003703	0.000	4.514
	TESTI4003944	0.000	35.590
	TESTI4004210	36.051	0.000
35	TESTI4005399	7.797	15.910
	TESTI4005653	1.989	3.551

	TESTI4006441	60.471	0.000
	TESTI4014908	36.051	0.000
	TESTI4022158	53.386	13.617
	TESTI4029297	0.000	4.514
5	THYMU3000776	15.604	0.000
	THYMU3002887	4.680	6.367
	THYMU3003007	0.000	19.391
	THYMU3003350	54.530	0.000
	THYMU3007308	0.000	39.793
10	THYMU3008105	0.000	20.662
	THYMU3021586	20.651	16.855
	THYMU3026000	49.066	0.000
	THYMU3026306	46.281	0.000
	THYMU3026350	14.291	14.581
15	THYMU3032798	9.668	0.000
	THYMU3032867	12.871	0.000
	THYMU3034671	0.000	4.866
	THYMU3037827	54.530	0.000
	THYMU3038214	39.314	0.000
20	THYMU3044075	37.925	19.346
	TKIDN2000319	0.000	21.607
	TRACH2013585	23.471	23.946
	TRACH3002752	10.215	10.422
	TRACH3003037	64.100	0.000
25	TRACH3003872	2.745	5.600
	TRACH3004424	17.006	0.000
	TRACH3006717	18.347	11.231
	TRACH3007625	1.175	10.794
	TRACH3007689	47.167	0.000
30	TRACH3008632	25.351	8.621
	TRACH3009008	24.495	0.000
	TRACH3010079	48.305	24.641
	TRACH3016805	4.502	0.000
	TRACH3016885	3.978	4.059
35	TRACH3022198	0.000	8.480
	TRACH3024342	47.167	0.000

	TRACH3024671	47.167	0.000
	TRACH3025316	0.000	31.291
	TRACH3026303	5.605	11.436
	TRACH3026676	11.631	0.000
5	TRACH3028855	22.309	0.000
	TRACH3032570	47.167	0.000
	TRACH3036932	14.659	14.956
	TRACH3038399	12.435	0.000
	TSTOM2000235	0.000	4.535
10	UTERU3005422	0.000	21.641
	UTERU3010409	3.461	7.062
	UTERU3013167	45.606	0.000
	UTERU3016273	0.000	46.104
	BRACE3046450	21.984	0.000
15	BRAWH3013197	100.000	0.000
	BRAWH3028645	100.000	0.000
	BRTHA3004432	32.087	0.000
	TRACH1000193	21.722	0.000

20

The result of comparative analysis of cDNA libraries derived from the cerebellum (BRACE), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

25

Table 7

	Clone ID	BRAWH	BRACE
30	ASTRO2016114	14.497	0.000
	BRACE1000475	0.000	100.000
	BRACE2002392	0.000	3.670
	BRACE2003628	0.000	9.684
	BRACE2005991	0.000	100.000
35	BRACE2010336	0.000	9.658
	BRACE2012528	3.794	15.820

	BRACE2012625	0.000	100.000
	BRACE2012833	0.000	100.000
	BRACE2012838	0.000	100.000
	BRACE2012936	0.000	100.000
5	BRACE2012947	0.000	100.000
	BRACE2013009	0.000	100.000
	BRACE2013126	0.000	100.000
	BRACE2013132	0.000	100.000
	BRACE2016896	0.000	100.000
10	BRACE2017359	0.000	58.183
	BRACE2017397	0.000	3.348
	BRACE2017580	0.000	100.000
	BRACE2017844	0.000	29.179
	BRACE2017872	0.000	100.000
15	BRACE2017992	0.000	100.000
	BRACE2019348	0.000	74.228
	BRACE2023633	0.000	100.000
	BRACE2023744	0.000	100.000
	BRACE2025452	0.000	100.000
20	BRACE2026404	0.000	100.000
	BRACE2027312	0.000	100.000
	BRACE2027382	0.000	100.000
	BRACE2028956	0.000	100.000
	BRACE2030039	0.000	100.000
25	BRACE2032584	0.000	100.000
	BRACE2033128	0.000	100.000
	BRACE2034434	0.000	100.000
	BRACE2035120	0.000	100.000
	BRACE2035191	0.000	100.000
30	BRACE2039362	0.000	100.000
	BRACE2039607	0.000	100.000
	BRACE2042541	0.000	100.000
	BRACE2046976	0.000	100.000
	BRACE2047232	0.000	100.000
35	BRACE2047975	0.000	100.000
	BRACE3001403	0.000	100.000

	BRACE3001973	0.000	36.360
	BRACE3002344	0.000	100.000
	BRACE3002541	0.000	100.000
	BRACE3002756	0.000	100.000
5	BRACE3003866	0.000	100.000
	BRACE3004046	0.000	41.027
	BRACE3004371	11.270	10.666
	BRACE3004767	58.488	41.512
	BRACE3004887	0.000	100.000
10	BRACE3004981	0.000	100.000
	BRACE3005870	0.000	100.000
	BRACE3005903	0.000	100.000
	BRACE3006553	0.000	18.271
	BRACE3007649	0.000	100.000
15	BRACE3007869	0.000	100.000
	BRACE3009075	0.000	100.000
	BRACE3009265	0.000	100.000
	BRACE3009392	0.000	100.000
	BRACE3009416	0.000	20.257
20	BRACE3009539	0.000	100.000
	BRACE3010702	0.000	100.000
	BRACE3011447	0.000	100.000
	BRACE3011774	0.000	100.000
	BRACE3013418	0.000	100.000
25	BRACE3013874	0.000	100.000
	BRACE3013986	0.000	100.000
	BRACE3014523	0.000	100.000
	BRACE3014714	0.000	100.000
	BRACE3015090	0.000	100.000
30	BRACE3015898	0.000	100.000
	BRACE3016020	0.000	100.000
	BRACE3016167	0.000	100.000
	BRACE3016580	0.000	100.000
	BRACE3016788	0.000	100.000
35	BRACE3016810	0.000	100.000
	BRACE3016862	0.000	100.000

	BRACE3017253	0.000	55.894
	BRACE3018083	0.000	100.000
	BRACE3019570	0.000	100.000
	BRACE3019611	0.000	100.000
5	BRACE3019817	0.000	100.000
	BRACE3019941	0.000	2.074
	BRACE3020356	0.000	100.000
	BRACE3020669	0.000	38.787
	BRACE3021430	0.000	8.467
10	BRACE3021517	0.000	100.000
	BRACE3021805	0.000	100.000
	BRACE3022051	0.000	100.000
	BRACE3022303	0.000	100.000
	BRACE3022312	0.000	24.151
15	BRACE3022340	58.488	41.512
	BRACE3022847	0.000	100.000
	BRACE3023604	0.000	100.000
	BRACE3024379	0.000	100.000
	BRACE3024444	0.000	100.000
20	BRACE3024497	0.000	100.000
	BRACE3024537	0.000	100.000
	BRACE3024879	0.000	100.000
	BRACE3025627	0.000	100.000
	BRACE3025719	0.000	12.784
25	BRACE3026161	0.000	100.000
	BRACE3026290	0.000	100.000
	BRACE3026345	0.000	100.000
	BRACE3026456	0.000	100.000
	BRACE3026802	0.000	36.390
30	BRACE3026844	0.000	100.000
	BRACE3026947	0.000	100.000
	BRACE3027256	0.000	100.000
	BRACE3027931	0.000	23.879
	BRACE3028360	0.000	100.000
35	BRACE3028895	0.000	32.302
	BRACE3028998	0.000	100.000

	BRACE3029005	0.000	100.000
	BRACE3029021	0.000	25.807
	BRACE3029205	0.000	100.000
	BRACE3029447	0.000	100.000
5	BRACE3030538	0.000	36.360
	BRACE3031161	0.000	100.000
	BRACE3031184	0.000	100.000
	BRACE3031185	58.488	41.512
	BRACE3031315	0.000	41.329
10	BRACE3031372	0.000	100.000
	BRACE3031579	0.000	100.000
	BRACE3031728	0.000	100.000
	BRACE3031743	5.455	15.488
	BRACE3031843	0.000	100.000
15	BRACE3032385	13.674	19.411
	BRACE3032537	0.000	100.000
	BRACE3032538	0.000	100.000
	BRACE3032631	12.612	8.951
	BRACE3032980	0.000	100.000
20	BRACE3033525	0.000	100.000
	BRACE3034183	0.000	100.000
	BRACE3034389	0.000	100.000
	BRACE3034964	0.000	100.000
	BRACE3034993	0.000	100.000
25	BRACE3035168	0.000	29.854
	BRACE3036156	0.000	31.069
	BRACE3036271	0.000	100.000
	BRACE3036283	0.000	5.298
	BRACE3037612	0.000	100.000
30	BRACE3037637	0.000	100.000
	BRACE3037803	0.000	100.000
	BRACE3038012	0.000	100.000
	BRACE3038030	0.000	100.000
	BRACE3038570	0.000	100.000
35	BRACE3038760	0.000	100.000
	BRACE3039288	0.000	100.000

	BRACE3039358	41.331	14.668
	BRACE3039378	0.000	100.000
	BRACE3039454	0.000	100.000
	BRACE3040012	0.000	100.000
5	BRACE3040239	0.000	100.000
	BRACE3040504	0.000	100.000
	BRACE3040644	0.000	100.000
	BRACE3040863	17.888	12.696
	BRACE3041059	0.000	100.000
10	BRACE3041162	0.000	100.000
	BRACE3041827	0.000	100.000
	BRACE3042046	0.000	100.000
	BRACE3042210	0.000	100.000
	BRACE3042326	0.000	24.903
15	BRACE3042409	0.000	100.000
	BRACE3042432	58.488	41.512
	BRACE3042594	0.000	100.000
	BRACE3043597	0.000	100.000
	BRACE3044090	0.000	100.000
20	BRACE3044172	0.000	100.000
	BRACE3044247	0.000	100.000
	BRACE3044377	0.000	100.000
	BRACE3044495	0.000	100.000
	BRACE3045078	0.000	58.183
25	BRACE3045145	0.000	100.000
	BRACE3045424	0.000	100.000
	BRACE3045708	0.000	100.000
	BRACE3045981	26.434	56.286
	BRACE3046049	0.000	100.000
30	BRACE3046152	0.000	100.000
	BRACE3046294	0.000	100.000
	BRACE3046466	0.000	100.000
	BRACE3046491	0.000	100.000
	BRACE3046609	0.000	100.000
35	BRACE3046837	0.000	100.000
	BRACE3046855	0.000	100.000

	BRACE3046966	0.000	100.000
	BRACE3047018	0.000	100.000
	BRACE3047482	0.000	100.000
	BRACE3047801	0.000	100.000
5	BRAMY2031516	14.772	0.000
	BRAMY3002329	20.323	9.616
	BRAMY3004126	49.811	0.000
	BRAMY3004364	0.000	4.821
	BRAMY3005912	21.416	30.401
10	BRAMY3008436	5.603	5.965
	BRAMY3009491	0.000	22.146
	BRAWH2000256	100.000	0.000
	BRAWH2002333	100.000	0.000
	BRAWH2004078	10.539	3.740
15	BRAWH2010364	34.464	36.692
	BRAWH2010619	100.000	0.000
	BRAWH2011796	100.000	0.000
	BRAWH2011812	13.544	0.000
	BRAWH2011958	100.000	0.000
20	BRAWH2012054	100.000	0.000
	BRAWH2012866	8.503	3.017
	BRAWH2013955	100.000	0.000
	BRAWH2014053	23.222	16.482
	BRAWH2016209	8.306	11.791
25	BRAWH2016223	100.000	0.000
	BRAWH2016305	4.308	0.000
	BRAWH2016514	35.037	0.000
	BRAWH2016562	49.499	0.000
	BRAWH2016785	100.000	0.000
30	BRAWH3000446	100.000	0.000
	BRAWH3000884	100.000	0.000
	BRAWH3001053	100.000	0.000
	BRAWH3001638	100.000	0.000
	BRAWH3001783	100.000	0.000
35	BRAWH3001833	100.000	0.000
	BRAWH3003244	100.000	0.000

	BRAWH3003573	20.162	14.310
	BRAWH3003975	100.000	0.000
	BRAWH3004335	100.000	0.000
	BRAWH3004350	16.580	0.000
5	BRAWH3005037	100.000	0.000
	BRAWH3005886	100.000	0.000
	BRAWH3005892	100.000	0.000
	BRAWH3005896	100.000	0.000
	BRAWH3008167	100.000	0.000
10	BRAWH3008559	100.000	0.000
	BRAWH3008867	100.000	0.000
	BRAWH3009961	47.417	0.000
	BRAWH3010461	16.435	10.207
	BRAWH3010602	100.000	0.000
15	BRAWH3010657	100.000	0.000
	BRAWH3010726	100.000	0.000
	BRAWH3010833	100.000	0.000
	BRAWH3011101	100.000	0.000
	BRAWH3011331	100.000	0.000
20	BRAWH3011402	100.000	0.000
	BRAWH3011577	100.000	0.000
	BRAWH3011623	100.000	0.000
	BRAWH3011685	100.000	0.000
	BRAWH3011907	47.417	0.000
25	BRAWH3011929	100.000	0.000
	BRAWH3012005	100.000	0.000
	BRAWH3012662	33.972	0.000
	BRAWH3012779	100.000	0.000
	BRAWH3013009	100.000	0.000
30	BRAWH3013049	100.000	0.000
	BRAWH3013264	100.000	0.000
	BRAWH3013508	100.000	0.000
	BRAWH3014609	44.597	0.000
	BRAWH3014639	100.000	0.000
35	BRAWH3015017	100.000	0.000
	BRAWH3015175	100.000	0.000

	BRAWH3015610	100.000	0.000
	BRAWH3015825	100.000	0.000
	BRAWH3016123	100.000	0.000
	BRAWH3016715	100.000	0.000
5	BRAWH3017180	28.251	40.103
	BRAWH3017259	13.996	4.967
	BRAWH3017260	100.000	0.000
	BRAWH3017477	100.000	0.000
	BRAWH3017980	49.811	0.000
10	BRAWH3018063	15.836	0.000
	BRAWH3018369	100.000	0.000
	BRAWH3018548	100.000	0.000
	BRAWH3018969	100.000	0.000
	BRAWH3019026	100.000	0.000
15	BRAWH3019529	100.000	0.000
	BRAWH3019594	100.000	0.000
	BRAWH3019820	100.000	0.000
	BRAWH3020200	100.000	0.000
	BRAWH3020318	100.000	0.000
20	BRAWH3020884	100.000	0.000
	BRAWH3020928	49.499	0.000
	BRAWH3021012	100.000	0.000
	BRAWH3021574	9.400	3.336
	BRAWH3021580	100.000	0.000
25	BRAWH3021641	100.000	0.000
	BRAWH3021643	100.000	0.000
	BRAWH3021724	100.000	0.000
	BRAWH3022347	100.000	0.000
	BRAWH3022431	100.000	0.000
30	BRAWH3022459	100.000	0.000
	BRAWH3022542	100.000	0.000
	BRAWH3022651	9.828	1.163
	BRAWH3022719	100.000	0.000
	BRAWH3022900	100.000	0.000
35	BRAWH3023156	100.000	0.000
	BRAWH3023168	100.000	0.000

	BRAWH3023172	0.916	0.000
	BRAWH3023274	100.000	0.000
	BRAWH3023421	100.000	0.000
	BRAWH3024186	19.959	0.000
5	BRAWH3024231	100.000	0.000
	BRAWH3024242	31.843	0.000
	BRAWH3024506	100.000	0.000
	BRAWH3024989	2.369	0.000
	BRAWH3026349	100.000	0.000
10	BRAWH3026938	6.894	4.893
	BRAWH3027420	100.000	0.000
	BRAWH3027440	58.488	41.512
	BRAWH3027533	11.008	0.000
	BRAWH3027574	47.417	0.000
15	BRAWH3027607	100.000	0.000
	BRAWH3027616	100.000	0.000
	BRAWH3027675	100.000	0.000
	BRAWH3027806	100.000	0.000
	BRAWH3027880	100.000	0.000
20	BRAWH3028202	100.000	0.000
	BRAWH3028223	100.000	0.000
	BRAWH3028461	100.000	0.000
	BRAWH3028754	100.000	0.000
	BRAWH3028796	100.000	0.000
25	BRAWH3029313	100.000	0.000
	BRAWH3029385	35.187	12.487
	BRAWH3029538	100.000	0.000
	BRAWH3029806	26.735	0.000
	BRAWH3030772	100.000	0.000
30	BRAWH3030810	21.287	67.989
	BRAWH3030910	100.000	0.000
	BRAWH3031054	100.000	0.000
	BRAWH3031342	10.856	7.705
	BRAWH3031710	100.000	0.000
35	BRAWH3032298	100.000	0.000
	BRAWH3032340	100.000	0.000

	BRAWH3032571	100.000	0.000
	BRAWH3033117	100.000	0.000
	BRAWH3033293	100.000	0.000
	BRAWH3033448	100.000	0.000
5	BRAWH3033513	100.000	0.000
	BRAWH3034097	100.000	0.000
	BRAWH3034114	100.000	0.000
	BRAWH3034134	100.000	0.000
	BRAWH3034668	100.000	0.000
10	BRAWH3034743	16.662	5.913
	BRAWH3034775	100.000	0.000
	BRAWH3034890	100.000	0.000
	BRAWH3035403	35.337	25.081
	BRAWH3035904	100.000	0.000
15	BRAWH3035914	100.000	0.000
	BRAWH3035936	70.575	0.000
	BRAWH3036077	100.000	0.000
	BRAWH3036247	54.530	0.000
	BRAWH3036270	100.000	0.000
20	BRAWH3036334	6.241	4.430
	BRAWH3036561	100.000	0.000
	BRAWH3037265	44.597	0.000
	BRAWH3037394	100.000	0.000
	BRAWH3037428	5.877	25.026
25	BRAWH3037533	100.000	0.000
	BRAWH3037979	100.000	0.000
	BRAWH3038055	100.000	0.000
	BRAWH3038230	100.000	0.000
	BRAWH3038252	100.000	0.000
30	BRAWH3038324	100.000	0.000
	BRCAN2010665	19.610	0.000
	BRCAN2019953	0.000	6.751
	BRCAN2022126	4.855	3.446
	BRCAN2025093	21.732	0.000
35	BRCOC2012386	11.403	0.000
	BRHIP2015153	20.038	14.222

	BRHIP2027077	2.020	0.000
	BRHIP2029643	0.000	10.603
	BRHIP3001360	0.000	41.027
	BRHIP3001573	24.474	0.000
5	BRHIP3002000	4.500	0.532
	BRHIP3002114	0.000	27.684
	BRHIP3003063	10.960	0.000
	BRHIP3003126	0.000	25.807
	BRHIP3003961	0.000	13.462
10	BRHIP3003984	27.477	29.254
	BRHIP3004215	0.000	9.636
	BRHIP3004774	39.520	0.000
	BRHIP3005801	0.000	13.302
	BRHIP3007223	2.016	1.431
15	BRHIP3007409	31.957	0.000
	BRHIP3008320	23.349	0.000
	BRHIP3014675	37.925	26.918
	BRHIP3017855	15.316	13.588
	BRHIP3018784	6.930	0.000
20	BRHIP3021019	7.745	0.000
	BRHIP3028246	22.147	0.000
	BRHIP3028570	31.957	0.000
	BRSSN2011843	0.000	8.495
	BRSSN2013696	0.000	12.675
25	BRSTN2010089	6.598	4.683
	BRSTN2011961	0.000	3.083
	BRSTN2012069	0.047	0.517
	BRSTN2016992	1.476	5.588
	BRTHA2033155	4.253	9.056
30	BRTHA2035743	0.000	4.816
	BRTHA3003736	4.302	1.527
	BRTHA3005988	31.076	0.000
	BRTHA3009858	0.000	16.462
	BRTHA3010135	20.010	0.000
35	BRTHA3010212	5.525	0.000
	BRTHA3010530	0.000	19.846

	BRTHA3011194	3.534	0.000
	BRTHA3011265	25.596	0.000
	BRTHA3011998	0.000	56.141
	BRTHA3017791	11.821	9.229
5	BRTHA3020771	31.957	0.000
	BRTHA3021708	0.000	39.025
	BRTHA3021971	1.941	0.000
	BRTHA3023403	14.857	0.000
	CHONS2002829	0.000	1.160
10	CTONG2006235	9.828	1.163
	CTONG2009033	25.755	0.000
	CTONG2020582	9.594	1.362
	CTONG2027959	0.000	27.592
	D90ST2003106	6.904	0.000
15	DFNES2001829	9.228	6.550
	KIDNE2010049	3.438	0.000
	KIDNE2017153	0.000	16.915
	LIVER2008465	0.000	4.697
	MESAN2017133	17.548	0.000
20	NOVAR2000783	0.000	2.684
	NT2RI2009233	6.767	1.601
	NT2RI2015533	6.216	3.309
	NT2RI3005923	19.493	0.000
	NT2RI3009524	35.496	0.000
25	NT2RP7007387	6.158	0.000
	NT2RP8001605	29.324	0.000
	NT2RP8007920	1.978	1.404
	NT2RP8009119	0.000	3.276
	NTONG2008483	2.397	0.000
30	NTONG2009468	0.000	13.482
	OCBBF2003518	2.062	0.000
	OCBBF2014745	0.000	36.360
	OCBBF2018618	16.218	0.000
	OCBBF3001333	9.639	4.561
35	OCBBF3004487	4.531	6.432
	PLACE7004103	3.880	0.918

	PLACE7006240	25.174	0.000
	PROST2007444	4.374	5.433
	TBAES2007428	5.371	0.000
	TESTI2005112	19.455	0.000
5	TESTI2018867	0.000	4.042
	TESTI2021654	9.773	0.000
	TESTI4002072	16.696	11.850
	TESTI4002774	4.103	0.000
	TESTI4002799	1.767	0.627
10	TESTI4003602	25.967	18.431
	TESTI4003703	0.000	6.281
	TESTI4004210	36.051	0.000
	TESTI4005013	0.000	11.599
	TESTI4005399	7.797	11.068
15	TESTI4005653	1.989	1.059
	TESTI4006441	60.471	0.000
	TESTI4014908	36.051	0.000
	TESTI4022158	53.386	9.473
	TESTI4029297	0.000	6.281
20	TESTI4032913	0.000	5.753
	TESTI4043223	0.000	19.643
	THYMU3000776	15.604	22.150
	THYMU3002887	4.680	7.197
	THYMU3003350	54.530	0.000
25	THYMU3007308	0.000	27.684
	THYMU3021586	20.651	0.000
	THYMU3026000	49.066	0.000
	THYMU3026306	46.281	0.000
	THYMU3026350	14.291	0.000
30	THYMU3032798	9.668	10.979
	THYMU3032867	12.871	9.135
	THYMU3033626	0.000	7.979
	THYMU3034671	0.000	5.078
	THYMU3037827	54.530	0.000
35	THYMU3038214	39.314	27.904
	THYMU3044075	37.925	26.918

	TLIVE2007736	0.000	9.358
	TRACH2013585	23.471	0.000
	TRACH3002752	10.215	3.625
	TRACH3003037	64.100	0.000
5	TRACH3003872	2.745	0.000
	TRACH3004424	17.006	0.000
	TRACH3006717	18.347	10.418
	TRACH3007625	1.175	2.503
	TRACH3007689	47.167	0.000
10	TRACH3007995	0.000	38.787
	TRACH3008632	25.351	11.995
	TRACH3009008	24.495	0.000
	TRACH3010079	48.305	0.000
	TRACH3016805	4.502	3.196
15	TRACH3016885	3.978	5.647
	TRACH3024342	47.167	0.000
	TRACH3024671	47.167	0.000
	TRACH3026303	5.605	0.000
	TRACH3026676	11.631	0.000
20	TRACH3028855	22.309	0.000
	TRACH3032570	47.167	0.000
	TRACH3036932	14.659	10.405
	TRACH3038399	12.435	8.826
	UTERU3000670	0.000	16.553
25	UTERU3010409	3.461	17.196
	UTERU3013167	45.606	0.000
	UTERU3015011	0.000	5.009
	BRACE3002184	0.000	19.020
	BRACE3026993	0.000	100.000
30	BRACE3046450	21.984	78.016
	BRAMY3008096	0.000	41.329
	BRAWH3013197	100.000	0.000
	BRAWH3028645	100.000	0.000
	BRTHA3004432	32.087	0.000
35	TESTI4002988	0.000	15.392
	TRACH1000193	21.722	15.417

The result of comparative analysis of cDNA libraries derived from the thalamus (BRTHA), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 8

	Clone ID	BRAWH	BRTHA
10	ASTR02008972	0.000	17.271
	ASTR02016114	14.497	0.000
	BLADE2004849	0.000	8.220
15	BRACE2002392	0.000	1.911
	BRACE2012528	3.794	13.673
	BRACE2019348	0.000	25.772
	BRACE3004371	11.270	4.166
	BRACE3004767	58.488	0.000
20	BRACE3019941	0.000	6.480
	BRACE3022312	0.000	37.734
	BRACE3022340	58.488	0.000
	BRACE3031185	58.488	0.000
	BRACE3031743	5.455	0.000
25	BRACE3032385	13.674	15.164
	BRACE3032631	12.612	0.000
	BRACE3036156	0.000	24.272
	BRACE3039358	41.331	22.917
	BRACE3040863	17.888	0.000
30	BRACE3042432	58.488	0.000
	BRACE3045981	26.434	0.000
	BRAMY2031516	14.772	0.000
	BRAMY3002329	20.323	15.025
	BRAMY3004126	49.811	0.000
35	BRAMY3005912	21.416	0.000
	BRAMY3008436	5.603	12.427

	BRAMY3009556	0.000	52.395
	BRAMY3010654	0.000	52.395
	BRAMY4001863	0.000	16.612
	BRAWH2000256	100.000	0.000
5	BRAWH2002333	100.000	0.000
	BRAWH2004078	10.539	0.000
	BRAWH2010364	34.464	0.000
	BRAWH2010619	100.000	0.000
	BRAWH2011796	100.000	0.000
10	BRAWH2011812	13.544	0.000
	BRAWH2011958	100.000	0.000
	BRAWH2012054	100.000	0.000
	BRAWH2012866	8.503	11.786
	BRAWH2013955	100.000	0.000
15	BRAWH2014053	23.222	25.752
	BRAWH2016209	8.306	0.000
	BRAWH2016223	100.000	0.000
	BRAWH2016305	4.308	0.000
	BRAWH2016514	35.037	0.000
20	BRAWH2016562	49.499	0.000
	BRAWH2016785	100.000	0.000
	BRAWH3000446	100.000	0.000
	BRAWH3000884	100.000	0.000
	BRAWH3001053	100.000	0.000
25	BRAWH3001638	100.000	0.000
	BRAWH3001783	100.000	0.000
	BRAWH3001833	100.000	0.000
	BRAWH3003244	100.000	0.000
	BRAWH3003573	20.162	22.358
30	BRAWH3003975	100.000	0.000
	BRAWH3004335	100.000	0.000
	BRAWH3004350	16.580	18.386
	BRAWH3005037	100.000	0.000
	BRAWH3005886	100.000	0.000
35	BRAWH3005892	100.000	0.000
	BRAWH3005896	100.000	0.000

	BRAWH3008167	100.000	0.000
	BRAWH3008559	100.000	0.000
	BRAWH3008867	100.000	0.000
	BRAWH3009961	47.417	52.583
5	BRAWH3010461	16.435	11.391
	BRAWH3010602	100.000	0.000
	BRAWH3010657	100.000	0.000
	BRAWH3010726	100.000	0.000
	BRAWH3010833	100.000	0.000
10	BRAWH3011101	100.000	0.000
	BRAWH3011331	100.000	0.000
	BRAWH3011402	100.000	0.000
	BRAWH3011577	100.000	0.000
	BRAWH3011623	100.000	0.000
15	BRAWH3011685	100.000	0.000
	BRAWH3011907	47.417	52.583
	BRAWH3011929	100.000	0.000
	BRAWH3012005	100.000	0.000
	BRAWH3012662	33.972	12.558
20	BRAWH3012779	100.000	0.000
	BRAWH3013009	100.000	0.000
	BRAWH3013049	100.000	0.000
	BRAWH3013264	100.000	0.000
	BRAWH3013508	100.000	0.000
25	BRAWH3014609	44.597	0.000
	BRAWH3014639	100.000	0.000
	BRAWH3015017	100.000	0.000
	BRAWH3015175	100.000	0.000
	BRAWH3015610	100.000	0.000
30	BRAWH3015825	100.000	0.000
	BRAWH3016123	100.000	0.000
	BRAWH3016715	100.000	0.000
	BRAWH3017180	28.251	0.000
	BRAWH3017259	13.996	0.000
35	BRAWH3017260	100.000	0.000
	BRAWH3017477	100.000	0.000

	BRAWH3017980	49.811	0.000
	BRAWH3018063	15.836	0.000
	BRAWH3018369	100.000	0.000
	BRAWH3018548	100.000	0.000
5	BRAWH3018969	100.000	0.000
	BRAWH3019026	100.000	0.000
	BRAWH3019529	100.000	0.000
	BRAWH3019594	100.000	0.000
	BRAWH3019820	100.000	0.000
10	BRAWH3020200	100.000	0.000
	BRAWH3020318	100.000	0.000
	BRAWH3020884	100.000	0.000
	BRAWH3020928	49.499	0.000
	BRAWH3021012	100.000	0.000
15	BRAWH3021574	9.400	0.000
	BRAWH3021580	100.000	0.000
	BRAWH3021641	100.000	0.000
	BRAWH3021643	100.000	0.000
	BRAWH3021724	100.000	0.000
20	BRAWH3022347	100.000	0.000
	BRAWH3022431	100.000	0.000
	BRAWH3022459	100.000	0.000
	BRAWH3022542	100.000	0.000
	BRAWH3022651	9.828	5.450
25	BRAWH3022719	100.000	0.000
	BRAWH3022900	100.000	0.000
	BRAWH3023156	100.000	0.000
	BRAWH3023168	100.000	0.000
	BRAWH3023172	0.916	2.031
30	BRAWH3023274	100.000	0.000
	BRAWH3023421	100.000	0.000
	BRAWH3024186	19.959	0.000
	BRAWH3024231	100.000	0.000
	BRAWH3024242	31.843	0.000
35	BRAWH3024506	100.000	0.000
	BRAWH3024989	2.369	0.000

	BRAWH3026349	100.000	0.000
	BRAWH3026938	6.894	0.000
	BRAWH3027420	100.000	0.000
	BRAWH3027440	58.488	0.000
5	BRAWH3027533	11.008	0.000
	BRAWH3027574	47.417	52.583
	BRAWH3027607	100.000	0.000
	BRAWH3027616	100.000	0.000
	BRAWH3027675	100.000	0.000
10	BRAWH3027806	100.000	0.000
	BRAWH3027880	100.000	0.000
	BRAWH3028202	100.000	0.000
	BRAWH3028223	100.000	0.000
	BRAWH3028461	100.000	0.000
15	BRAWH3028754	100.000	0.000
	BRAWH3028796	100.000	0.000
	BRAWH3029313	100.000	0.000
	BRAWH3029385	35.187	0.000
	BRAWH3029538	100.000	0.000
20	BRAWH3029806	26.735	9.883
	BRAWH3030772	100.000	0.000
	BRAWH3030810	21.287	0.000
	BRAWH3030910	100.000	0.000
	BRAWH3031054	100.000	0.000
25	BRAWH3031342	10.856	0.000
	BRAWH3031710	100.000	0.000
	BRAWH3032298	100.000	0.000
	BRAWH3032340	100.000	0.000
	BRAWH3032571	100.000	0.000
30	BRAWH3033117	100.000	0.000
	BRAWH3033293	100.000	0.000
	BRAWH3033448	100.000	0.000
	BRAWH3033513	100.000	0.000
	BRAWH3034097	100.000	0.000
35	BRAWH3034114	100.000	0.000
	BRAWH3034134	100.000	0.000

	BRAWH3034668	100.000	0.000
	BRAWH3034743	16.662	18.478
	BRAWH3034775	100.000	0.000
	BRAWH3034890	100.000	0.000
5	BRAWH3035403	35.337	0.000
	BRAWH3035904	100.000	0.000
	BRAWH3035914	100.000	0.000
	BRAWH3035936	70.575	0.000
	BRAWH3036077	100.000	0.000
10	BRAWH3036247	54.530	0.000
	BRAWH3036270	100.000	0.000
	BRAWH3036334	6.241	6.921
	BRAWH3036561	100.000	0.000
	BRAWH3037265	44.597	0.000
15	BRAWH3037394	100.000	0.000
	BRAWH3037428	5.877	19.551
	BRAWH3037533	100.000	0.000
	BRAWH3037979	100.000	0.000
	BRAWH3038055	100.000	0.000
20	BRAWH3038230	100.000	0.000
	BRAWH3038252	100.000	0.000
	BRAWH3038324	100.000	0.000
	BRCAN2002892	0.000	32.586
	BRCAN2010665	19.610	7.249
25	BRCAN2020234	0.000	27.335
	BRCAN2022126	4.855	0.000
	BRCAN2025093	21.732	0.000
	BRCOC2006164	0.000	32.234
	BRCOC2012386	11.403	0.000
30	BRHIP2013958	0.000	39.849
	BRHIP2015153	20.038	0.000
	BRHIP2027077	2.020	0.000
	BRHIP3001573	24.474	27.141
	BRHIP3002000	4.500	0.832
35	BRHIP3002691	0.000	18.395
	BRHIP3002920	0.000	35.211

	BRHIP3003063	10.960	0.000
	BRHIP3003961	0.000	21.034
	BRHIP3003984	27.477	15.236
	BRHIP3004215	0.000	15.055
5	BRHIP3004774	39.520	0.000
	BRHIP3007223	2.016	4.472
	BRHIP3007409	31.957	35.439
	BRHIP3008320	23.349	0.000
	BRHIP3014675	37.925	0.000
10	BRHIP3017855	15.316	4.246
	BRHIP3018784	6.930	0.000
	BRHIP3020046	0.000	1.123
	BRHIP3021019	7.745	0.000
	BRHIP3028246	22.147	0.000
15	BRHIP3028570	31.957	35.439
	BRSSN2015497	0.000	7.931
	BRSTN2010089	6.598	0.000
	BRSTN2011961	0.000	1.285
	BRSTN2012069	0.047	0.000
20	BRSTN2016992	1.476	1.091
	BRTHA2000969	0.000	100.000
	BRTHA2001304	0.000	100.000
	BRTHA2001953	0.000	10.615
	BRTHA2002091	0.000	100.000
25	BRTHA2003759	0.000	100.000
	BRTHA2005448	0.000	100.000
	BRTHA2006720	0.000	100.000
	BRTHA2008502	0.000	23.993
	BRTHA2008598	0.000	100.000
30	BRTHA2010672	0.000	100.000
	BRTHA2012189	0.000	100.000
	BRTHA2014647	0.000	100.000
	BRTHA2018304	0.000	100.000
	BRTHA2019726	0.000	100.000
35	BRTHA2019743	0.000	100.000
	BRTHA2020400	0.000	100.000

	BRTHA2020566	0.000	100.000
	BRTHA2020642	0.000	100.000
	BRTHA2020695	0.000	100.000
	BRTHA2020721	0.000	100.000
5	BRTHA2020781	0.000	100.000
	BRTHA2020910	0.000	100.000
	BRTHA2021212	0.000	100.000
	BRTHA2021440	0.000	57.080
	BRTHA2021450	0.000	100.000
10	BRTHA2022074	0.000	100.000
	BRTHA2022914	0.000	100.000
	BRTHA2022968	0.000	100.000
	BRTHA2023402	0.000	100.000
	BRTHA2023437	0.000	100.000
15	BRTHA2024177	0.000	100.000
	BRTHA2024354	0.000	100.000
	BRTHA2024712	0.000	100.000
	BRTHA2025869	0.000	100.000
	BRTHA2026071	0.000	13.612
20	BRTHA2026290	0.000	100.000
	BRTHA2026311	0.000	100.000
	BRTHA2027227	0.000	100.000
	BRTHA2027229	0.000	2.030
	BRTHA2027250	0.000	100.000
25	BRTHA2028297	0.000	100.000
	BRTHA2029969	0.000	100.000
	BRTHA2030036	0.000	100.000
	BRTHA2030213	0.000	100.000
	BRTHA2031517	0.000	52.083
30	BRTHA2031917	0.000	100.000
	BRTHA2032763	0.000	100.000
	BRTHA2033122	0.000	100.000
	BRTHA2033155	4.253	9.433
	BRTHA2033320	0.000	100.000
35	BRTHA2033469	0.000	38.930
	BRTHA2033683	0.000	100.000

	BRTHA2034281	0.000	100.000
	BRTHA2034576	0.000	100.000
	BRTHA2035743	0.000	22.576
	BRTHA2036055	0.000	100.000
5	BRTHA2036295	0.000	100.000
	BRTHA2037247	0.000	100.000
	BRTHA2038279	0.000	100.000
	BRTHA2038345	0.000	100.000
	BRTHA2038353	0.000	100.000
10	BRTHA3000456	0.000	62.915
	BRTHA3002411	0.000	100.000
	BRTHA3003225	0.000	47.165
	BRTHA3003417	0.000	34.129
	BRTHA3003736	4.302	2.385
15	BRTHA3005988	31.076	68.924
	BRTHA3006593	0.000	100.000
	BRTHA3007469	0.000	100.000
	BRTHA3007662	0.000	35.211
	BRTHA3009858	0.000	25.720
20	BRTHA3010135	20.010	44.380
	BRTHA3010212	5.525	6.127
	BRTHA3010469	0.000	100.000
	BRTHA3010530	0.000	31.009
	BRTHA3010540	0.000	7.466
25	BRTHA3010717	0.000	100.000
	BRTHA3011187	0.000	100.000
	BRTHA3011194	3.534	3.920
	BRTHA3011229	0.000	100.000
	BRTHA3011265	25.596	18.923
30	BRTHA3011306	0.000	13.657
	BRTHA3011361	0.000	62.915
	BRTHA3011510	0.000	100.000
	BRTHA3011892	0.000	100.000
	BRTHA3011998	0.000	43.859
35	BRTHA3012265	0.000	35.211
	BRTHA3013860	0.000	100.000

	BRTHA3013882	0.000	100.000
	BRTHA3014000	0.000	100.000
	BRTHA3014105	0.000	100.000
	BRTHA3014507	0.000	100.000
5	BRTHA3014547	0.000	100.000
	BRTHA3014835	0.000	100.000
	BRTHA3014854	0.000	100.000
	BRTHA3014920	0.000	100.000
	BRTHA3016616	0.000	100.000
10	BRTHA3017791	11.821	5.244
	BRTHA3018409	0.000	100.000
	BRTHA3018623	0.000	100.000
	BRTHA3019183	0.000	100.000
	BRTHA3020369	0.000	100.000
15	BRTHA3020771	31.957	35.439
	BRTHA3021569	0.000	100.000
	BRTHA3021708	0.000	60.975
	BRTHA3021786	0.000	100.000
	BRTHA3021971	1.941	4.305
20	BRTHA3022641	0.000	19.618
	BRTHA3023403	14.857	8.238
	BRTHA3023590	0.000	100.000
	BRTHA3023929	0.000	100.000
	BRTHA3024600	0.000	100.000
25	BRTHA3025073	0.000	100.000
	BRTHA3026161	0.000	100.000
	BRTHA3026180	0.000	100.000
	BRTHA3026556	0.000	100.000
	BRTHA3026916	0.000	52.395
30	BRTHA3027171	0.000	100.000
	BRTHA3027318	0.000	100.000
	BRTHA3027638	0.000	100.000
	BRTHA3027820	0.000	100.000
	BRTHA3027879	0.000	48.181
35	BRTHA3027957	0.000	100.000
	BRTHA3028339	0.000	100.000

	BRTHA3028505	0.000	100.000
	CHONS2002829	0.000	1.812
	CTONG2006235	9.828	5.450
	CTONG2009033	25.755	0.000
5	CTONG2011801	0.000	3.284
	CTONG2020582	9.594	4.256
	D90ST2003106	6.904	0.000
	DFNES2001829	9.228	0.000
	KIDNE2010049	3.438	0.000
10	LIVER2008465	0.000	7.339
	MESAN2017133	17.548	0.000
	NT2RI2009233	6.767	2.501
	NT2RI2010795	0.000	36.581
	NT2RI2015533	6.216	12.064
15	NT2RI3005923	19.493	0.000
	NT2RI3009524	35.496	0.000
	NT2RP7007387	6.158	2.276
	NT2RP8001605	29.324	0.000
	NT2RP8007920	1.978	0.000
20	NTONG2008483	2.397	1.772
	OCBBF2003518	2.062	0.000
	OCBBF2009536	0.000	47.165
	OCBBF2018618	16.218	0.000
	OCBBF3001333	9.639	0.000
25	OCBBF3004487	4.531	0.000
	OCBBF3008835	0.000	47.165
	PLACE6003004	0.000	38.390
	PLACE7004103	3.880	4.302
	PLACE7006240	25.174	0.000
30	PROST2007444	4.374	3.638
	SMINT2009292	0.000	3.933
	TBAES2007428	5.371	0.000
	TESTI2005112	19.455	0.000
	TESTI2021654	9.773	10.838
35	TESTI2039342	0.000	77.236
	TESTI4002072	16.696	11.109

	TESTI4002774	4.103	0.000
	TESTI4002799	1.767	1.469
	TESTI4003602	25.967	0.000
	TESTI4003703	0.000	4.907
5	TESTI4004210	36.051	0.000
	TESTI4004695	0.000	36.122
	TESTI4005399	7.797	0.000
	TESTI4005653	1.989	0.551
	TESTI4006441	60.471	0.000
10	TESTI4007965	0.000	20.014
	TESTI4010979	0.000	21.790
	TESTI4013474	0.000	2.292
	TESTI4014908	36.051	0.000
	TESTI4022158	53.386	14.801
15	TESTI4029297	0.000	4.907
	TESTI4032913	0.000	8.989
	THYMU3000776	15.604	0.000
	THYMU3002887	4.680	3.460
	THYMU3003350	54.530	0.000
20	THYMU3021586	20.651	4.580
	THYMU3026000	49.066	0.000
	THYMU3026306	46.281	0.000
	THYMU3026350	14.291	15.849
	THYMU3032798	9.668	4.289
25	THYMU3032867	12.871	0.000
	THYMU3037827	54.530	0.000
	THYMU3038214	39.314	0.000
	THYMU3044075	37.925	0.000
	TRACH2013585	23.471	0.000
30	TRACH3002752	10.215	0.000
	TRACH3003037	64.100	0.000
	TRACH3003872	2.745	0.000
	TRACH3004424	17.006	18.859
	TRACH3006717	18.347	0.000
35	TRACH3007625	1.175	3.911
	TRACH3007689	47.167	0.000

	TRACH3008508	0.000	21.245
	TRACH3008632	25.351	9.371
	TRACH3009008	24.495	0.000
	TRACH3010079	48.305	0.000
5	TRACH3016805	4.502	0.000
	TRACH3016885	3.978	0.000
	TRACH3024342	47.167	0.000
	TRACH3024671	47.167	0.000
	TRACH3026303	5.605	0.000
10	TRACH3026676	11.631	12.899
	TRACH3028855	22.309	0.000
	TRACH3032570	47.167	0.000
	TRACH3036932	14.659	16.256
	TRACH3038399	12.435	13.790
15	UTERU3010409	3.461	0.000
	UTERU3012414	0.000	48.181
	UTERU3013167	45.606	0.000
	UTERU3017995	0.000	12.128
	UTERU3018172	0.000	35.368
20	BRA3046450	21.984	0.000
	BRAWH3013197	100.000	0.000
	BRAWH3028645	100.000	0.000
	BRTHA3004432	32.087	35.583
	BRTHA3024233	0.000	100.000
25	CTONG2002832	0.000	12.432
	THYMU3046350	0.000	15.320
	TRACH1000193	21.722	0.000

30 The result of comparative analysis of cDNA libraries derived from the amygdale (BRAMY), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 9

	Clone ID	BRAWH	BRAMY
5	ASTR02016114	14.497	0.000
	BRACE2002392	0.000	5.210
	BRACE2012528	3.794	10.512
	BRACE2017397	0.000	2.376
	BRACE2017844	0.000	15.534
10	BRACE3004371	11.270	7.571
	BRACE3004767	58.488	0.000
	BRACE3022340	58.488	0.000
	BRACE3031185	58.488	0.000
	BRACE3031315	0.000	58.671
15	BRACE3031743	5.455	5.497
	BRACE3032385	13.674	13.778
	BRACE3032631	12.612	0.000
	BRACE3039358	41.331	0.000
	BRACE3040863	17.888	0.000
20	BRACE3042432	58.488	0.000
	BRACE3045981	26.434	0.000
	BRAMY2015516	0.000	100.000
	BRAMY2021098	0.000	100.000
	BRAMY2022320	0.000	100.000
25	BRAMY2023939	0.000	6.159
	BRAMY2025495	0.000	100.000
	BRAMY2031516	14.772	7.442
	BRAMY2033895	0.000	100.000
	BRAMY2035801	0.000	100.000
30	BRAMY2036254	0.000	100.000
	BRAMY2036266	0.000	100.000
	BRAMY2037609	0.000	100.000
	BRAMY2039630	0.000	8.744
	BRAMY2040915	0.000	100.000
35	BRAMY2041347	0.000	100.000
	BRAMY2041384	0.000	100.000

	BRAMY2041507	0.000	100.000
	BRAMY2044686	0.000	100.000
	BRAMY2046489	0.000	100.000
	BRAMY2046537	0.000	100.000
5	BRAMY3000692	0.000	100.000
	BRAMY3001409	0.000	100.000
	BRAMY3002329	20.323	20.478
	BRAMY3002508	0.000	100.000
	BRAMY3002886	0.000	100.000
10	BRAMY3004126	49.811	50.189
	BRAMY3004364	0.000	13.689
	BRAMY3005184	0.000	22.578
	BRAMY3005656	0.000	100.000
	BRAMY3005912	21.416	21.579
15	BRAMY3007078	0.000	49.688
	BRAMY3007449	0.000	100.000
	BRAMY3007471	0.000	100.000
	BRAMY3008436	5.603	4.234
	BRAMY3009158	0.000	100.000
20	BRAMY3009491	0.000	31.439
	BRAMY3009556	0.000	47.605
	BRAMY3009904	0.000	100.000
	BRAMY3010321	0.000	100.000
	BRAMY3010603	0.000	100.000
25	BRAMY3010654	0.000	47.605
	BRAMY4000915	0.000	49.688
	BRAMY4000962	0.000	100.000
	BRAMY4001234	0.000	54.718
	BRAMY4001652	0.000	100.000
30	BRAMY4001863	0.000	15.094
	BRAMY4001913	0.000	100.000
	BRAMY4002575	0.000	100.000
	BRAMY4002628	0.000	7.157
	BRAWH2000256	100.000	0.000
35	BRAWH2002333	100.000	0.000
	BRAWH2004078	10.539	0.000

	BRAWH2010364	34.464	0.000
	BRAWH2010619	100.000	0.000
	BRAWH2011796	100.000	0.000
	BRAWH2011812	13.544	13.646
5	BRAWH2011958	100.000	0.000
	BRAWH2012054	100.000	0.000
	BRAWH2012866	8.503	14.993
	BRAWH2013955	100.000	0.000
	BRAWH2014053	23.222	0.000
10	BRAWH2016209	8.306	0.000
	BRAWH2016223	100.000	0.000
	BRAWH2016305	4.308	0.000
	BRAWH2016514	35.037	0.000
	BRAWH2016562	49.499	0.000
15	BRAWH2016785	100.000	0.000
	BRAWH3000446	100.000	0.000
	BRAWH3000884	100.000	0.000
	BRAWH3001053	100.000	0.000
	BRAWH3001638	100.000	0.000
20	BRAWH3001783	100.000	0.000
	BRAWH3001833	100.000	0.000
	BRAWH3003244	100.000	0.000
	BRAWH3003573	20.162	0.000
	BRAWH3003975	100.000	0.000
25	BRAWH3004335	100.000	0.000
	BRAWH3004350	16.580	0.000
	BRAWH3005037	100.000	0.000
	BRAWH3005886	100.000	0.000
	BRAWH3005892	100.000	0.000
30	BRAWH3005896	100.000	0.000
	BRAWH3008167	100.000	0.000
	BRAWH3008559	100.000	0.000
	BRAWH3008867	100.000	0.000
	BRAWH3009961	47.417	0.000
35	BRAWH3010461	16.435	14.490
	BRAWH3010602	100.000	0.000

	BRAWH3010657	100.000	0.000
	BRAWH3010726	100.000	0.000
	BRAWH3010833	100.000	0.000
	BRAWH3011101	100.000	0.000
5	BRAWH3011331	100.000	0.000
	BRAWH3011402	100.000	0.000
	BRAWH3011577	100.000	0.000
	BRAWH3011623	100.000	0.000
	BRAWH3011685	100.000	0.000
10	BRAWH3011907	47.417	0.000
	BRAWH3011929	100.000	0.000
	BRAWH3012005	100.000	0.000
	BRAWH3012662	33.972	0.000
	BRAWH3012779	100.000	0.000
15	BRAWH3013009	100.000	0.000
	BRAWH3013049	100.000	0.000
	BRAWH3013264	100.000	0.000
	BRAWH3013508	100.000	0.000
	BRAWH3014609	44.597	0.000
20	BRAWH3014639	100.000	0.000
	BRAWH3015017	100.000	0.000
	BRAWH3015175	100.000	0.000
	BRAWH3015610	100.000	0.000
	BRAWH3015825	100.000	0.000
25	BRAWH3016123	100.000	0.000
	BRAWH3016715	100.000	0.000
	BRAWH3017180	28.251	0.000
	BRAWH3017259	13.996	0.000
	BRAWH3017260	100.000	0.000
30	BRAWH3017477	100.000	0.000
	BRAWH3017980	49.811	50.189
	BRAWH3018063	15.836	7.978
	BRAWH3018369	100.000	0.000
	BRAWH3018548	100.000	0.000
35	BRAWH3018969	100.000	0.000
	BRAWH3019026	100.000	0.000

	BRAWH3019529	100.000	0.000
	BRAWH3019594	100.000	0.000
	BRAWH3019820	100.000	0.000
	BRAWH3020200	100.000	0.000
5	BRAWH3020318	100.000	0.000
	BRAWH3020884	100.000	0.000
	BRAWH3020928	49.499	0.000
	BRAWH3021012	100.000	0.000
	BRAWH3021574	9.400	0.000
10	BRAWH3021580	100.000	0.000
	BRAWH3021641	100.000	0.000
	BRAWH3021643	100.000	0.000
	BRAWH3021724	100.000	0.000
	BRAWH3022347	100.000	0.000
15	BRAWH3022431	100.000	0.000
	BRAWH3022459	100.000	0.000
	BRAWH3022542	100.000	0.000
	BRAWH3022651	9.828	4.952
	BRAWH3022719	100.000	0.000
20	BRAWH3022900	100.000	0.000
	BRAWH3023156	100.000	0.000
	BRAWH3023168	100.000	0.000
	BRAWH3023172	0.916	0.000
	BRAWH3023274	100.000	0.000
25	BRAWH3023421	100.000	0.000
	BRAWH3024186	19.959	10.055
	BRAWH3024231	100.000	0.000
	BRAWH3024242	31.843	0.000
	BRAWH3024506	100.000	0.000
30	BRAWH3024989	2.369	0.000
	BRAWH3026349	100.000	0.000
	BRAWH3026938	6.894	0.000
	BRAWH3027420	100.000	0.000
	BRAWH3027440	58.488	0.000
35	BRAWH3027533	11.008	0.000
	BRAWH3027574	47.417	0.000

	BRAWH3027607	100.000	0.000
	BRAWH3027616	100.000	0.000
	BRAWH3027675	100.000	0.000
	BRAWH3027806	100.000	0.000
5	BRAWH3027880	100.000	0.000
	BRAWH3028202	100.000	0.000
	BRAWH3028223	100.000	0.000
	BRAWH3028461	100.000	0.000
	BRAWH3028754	100.000	0.000
10	BRAWH3028796	100.000	0.000
	BRAWH3029313	100.000	0.000
	BRAWH3029385	35.187	0.000
	BRAWH3029538	100.000	0.000
	BRAWH3029806	26.735	8.979
15	BRAWH3030772	100.000	0.000
	BRAWH3030810	21.287	10.724
	BRAWH3030910	100.000	0.000
	BRAWH3031054	100.000	0.000
	BRAWH3031342	10.856	0.000
20	BRAWH3031710	100.000	0.000
	BRAWH3032298	100.000	0.000
	BRAWH3032340	100.000	0.000
	BRAWH3032571	100.000	0.000
	BRAWH3033117	100.000	0.000
25	BRAWH3033293	100.000	0.000
	BRAWH3033448	100.000	0.000
	BRAWH3033513	100.000	0.000
	BRAWH3034097	100.000	0.000
	BRAWH3034114	100.000	0.000
30	BRAWH3034134	100.000	0.000
	BRAWH3034668	100.000	0.000
	BRAWH3034743	16.662	12.592
	BRAWH3034775	100.000	0.000
	BRAWH3034890	100.000	0.000
35	BRAWH3035403	35.337	0.000
	BRAWH3035904	100.000	0.000

	BRAWH3035914	100.000	0.000
	BRAWH3035936	70.575	0.000
	BRAWH3036077	100.000	0.000
	BRAWH3036247	54.530	0.000
5	BRAWH3036270	100.000	0.000
	BRAWH3036334	6.241	0.000
	BRAWH3036561	100.000	0.000
	BRAWH3037265	44.597	0.000
	BRAWH3037394	100.000	0.000
10	BRAWH3037428	5.877	5.921
	BRAWH3037533	100.000	0.000
	BRAWH3037979	100.000	0.000
	BRAWH3038055	100.000	0.000
	BRAWH3038230	100.000	0.000
15	BRAWH3038252	100.000	0.000
	BRAWH3038324	100.000	0.000
	BRCAN2010665	19.610	9.879
	BRCAN2022126	4.855	14.677
	BRCAN2025093	21.732	0.000
20	BRCOC2012386	11.403	0.000
	BRHIP2015153	20.038	10.095
	BRHIP2027077	2.020	2.035
	BRHIP3001573	24.474	8.220
	BRHIP3002000	4.500	0.756
25	BRHIP3002691	0.000	8.357
	BRHIP3003063	10.960	33.130
	BRHIP3003984	27.477	0.000
	BRHIP3004215	0.000	13.679
	BRHIP3004774	39.520	0.000
30	BRHIP3005673	0.000	25.956
	BRHIP3007223	2.016	0.000
	BRHIP3007409	31.957	0.000
	BRHIP3008320	23.349	0.000
	BRHIP3012736	0.000	66.389
35	BRHIP3014675	37.925	0.000
	BRHIP3017146	0.000	33.057

	BRHIP3017855	15.316	0.000
	BRHIP3018784	6.930	0.000
	BRHIP3020046	0.000	1.021
	BRHIP3021019	7.745	7.803
5	BRHIP3028246	22.147	22.315
	BRHIP3028570	31.957	0.000
	BRSTN2010089	6.598	0.000
	BRSTN2012069	0.047	0.029
	BRSTN2016992	1.476	4.958
10	BRTHA2026071	0.000	12.368
	BRTHA2033155	4.253	4.285
	BRTHA3003736	4.302	0.000
	BRTHA3005988	31.076	0.000
	BRTHA3010135	20.010	0.000
15	BRTHA3010212	5.525	5.567
	BRTHA3011194	3.534	0.000
	BRTHA3011265	25.596	0.000
	BRTHA3017791	11.821	5.956
	BRTHA3020771	31.957	0.000
20	BRTHA3021971	1.941	1.956
	BRTHA3023403	14.857	7.485
	BRTHA3026916	0.000	47.605
	CHONS2002829	0.000	1.646
	CTONG2006235	9.828	4.952
25	CTONG2009033	25.755	0.000
	CTONG2020582	9.594	3.867
	D9OST2003106	6.904	0.000
	DFNES2001829	9.228	0.000
	KIDNE2010049	3.438	0.000
30	MESAN2017133	17.548	0.000
	NT2RI2009233	6.767	4.545
	NT2RI2010795	0.000	16.619
	NT2RI2015533	6.216	12.527
	NT2RI3005923	19.493	0.000
35	NT2RI3009524	35.496	0.000
	NT2RP7007387	6.158	0.000

	NT2RP8001605	29.324	0.000
	NT2RP8007920	1.978	0.000
	NTONG2008483	2.397	0.000
	OCBBF2000831	0.000	9.702
5	OCBBF2003518	2.062	1.039
	OCBBF2018618	16.218	16.341
	OCBBF2030927	0.000	44.784
	OCBBF3001333	9.639	6.475
	OCBBF3004487	4.531	4.565
10	OCBBF3009244	0.000	34.702
	PLACE6008315	0.000	1.403
	PLACE6010936	0.000	12.399
	PLACE7004103	3.880	1.303
	PLACE7006240	25.174	0.000
15	PROST2007444	4.374	1.102
	SPLEN2012571	0.000	3.203
	SYNOV4004210	0.000	0.952
	SYNOV4009575	0.000	4.828
	TBAES2007428	5.371	0.000
20	TESTI2005112	19.455	0.000
	TESTI2021654	9.773	9.847
	TESTI4002072	16.696	3.364
	TESTI4002774	4.103	0.000
	TESTI4002799	1.767	0.000
25	TESTI4003602	25.967	0.000
	TESTI4003703	0.000	4.458
	TESTI4004210	36.051	0.000
	TESTI4005399	7.797	15.713
	TESTI4005653	1.989	3.507
30	TESTI4006441	60.471	0.000
	TESTI4014908	36.051	0.000
	TESTI4022158	53.386	0.000
	TESTI4029297	0.000	4.458
	TESTI4032913	0.000	8.167
35	TESTI4043223	0.000	27.886
	TESTI4046073	0.000	19.130

	THYMU3000776	15.604	0.000
	THYMU3002887	4.680	3.930
	THYMU3003350	54.530	0.000
	THYMU3008105	0.000	20.406
5	THYMU3019476	0.000	54.718
	THYMU3021586	20.651	4.162
	THYMU3026000	49.066	0.000
	THYMU3026306	46.281	0.000
	THYMU3026350	14.291	14.400
10	THYMU3032798	9.668	1.948
	THYMU3032867	12.871	0.000
	THYMU3037827	54.530	0.000
	THYMU3038214	39.314	0.000
	THYMU3044075	37.925	0.000
15	TRACH2013585	23.471	0.000
	TRACH3002752	10.215	0.000
	TRACH3003037	64.100	0.000
	TRACH3003872	2.745	2.765
	TRACH3004424	17.006	0.000
20	TRACH3006717	18.347	3.697
	TRACH3007625	1.175	3.553
	TRACH3007689	47.167	0.000
	TRACH3008632	25.351	0.000
	TRACH3009008	24.495	0.000
25	TRACH3010079	48.305	0.000
	TRACH3016805	4.502	0.000
	TRACH3016885	3.978	12.025
	TRACH3024342	47.167	0.000
	TRACH3024671	47.167	0.000
30	TRACH3026303	5.605	0.000
	TRACH3026676	11.631	0.000
	TRACH3028855	22.309	0.000
	TRACH3032570	47.167	0.000
	TRACH3036932	14.659	0.000
35	TRACH3038399	12.435	0.000
	UTERU3010409	3.461	0.000

	UTERU3013167	45.606	0.000
	BRACE3046450	21.984	0.000
	BRAMY3008096	0.000	58.671
	BRAWH3013197	100.000	0.000
5	BRAWH3028645	100.000	0.000
	BRTHA3004432	32.087	32.330
	TESTI4002988	0.000	21.851
	THYMU3046350	0.000	6.960
	TRACH1000193	21.722	0.000
10	TRACH3019290	0.000	27.871

The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES), and normal breast (BEAST) showed the following genes whose expression levels differed between the two.

Table 10

	Clone ID	BEAST	TBAES
	BRSTN2011961	6.317	4.075
	BRSTN2012069	0.000	0.067
	TBAES2003917	0.000	100.000
25	TBAES2005361	0.000	100.000
	TBAES2007428	0.000	37.783
	TBAES2007548	0.000	100.000
	TBAES2007862	0.000	100.000
	TESTI2005564	0.000	25.762
30	TESTI4017854	0.000	91.498
	TRACH3016805	0.000	31.673
	TBAES2004105	0.000	100.000
	TBAES2007379	0.000	100.000
	TBAES2007481	0.000	100.000
35	TBAES2008133	0.000	100.000

The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX), and normal cervical duct (CERVX) showed the following genes whose expression levels differed between the two.

Table 11

Clone ID	CERVX	TCERX
BRACE2017397	48.741	0.000
BRHIP2027077	41.741	0.000
BRSTN2011961	5.985	0.000
BRSTN2012069	5.668	7.585
CERVX2000812	100.000	0.000
CERVX2000968	100.000	0.000

The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN), and normal colon (COLON) showed the following genes whose expression levels differed between the two.

Table 12

Clone ID	COLON	TCOLN
BRSTN2011961	0.000	6.140
BRSTN2012069	1.726	1.805
COLON2001829	100.000	0.000
COLON2001866	100.000	0.000
COLON2004351	100.000	0.000
COLON2004911	100.000	0.000
COLON2005623	100.000	0.000
COLON2005735	100.000	0.000
OCBBF3001333	22.556	0.000

SMINT2017964 34.030 0.000

5 The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP), and normal esophagus (NESOP) showed the following genes whose expression levels differed between the two.

Table 13

10	Clone ID	NESOP	TESOP
	BRAMY3004364	0.000	46.478
	BRAWH3027533	0.000	75.317
15	BRHIP3007223	42.899	0.000
	BRSTN2011961	0.000	1.981
	BRSTN2012069	1.409	2.071
	CTONG2011801	0.000	20.259
	CTONG3002518	0.000	57.732
20	SMINT2009292	0.000	24.268
	TESOP2002005	0.000	100.000
	TESOP2003308	0.000	100.000
	TESOP2004110	0.000	100.000
	TESOP2008556	0.000	100.000
25	UTERU3015011	0.000	48.286
	UTERU3017995	0.000	74.828

30 The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN), and normal kidney (KIDNE) showed the following genes whose expression levels differed between the two.

Table 14

35	Clone ID	KIDNE	TKIDN
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	BRACE2002392	0.000	6.380
	BRACE2012528	0.000	14.044
	BRACE3004371	13.097	0.000
5	BRAMY2039630	60.511	0.000
	BRAMY3004364	23.683	0.000
	BRAMY3008436	0.000	5.185
	BRAWH2004078	18.371	0.000
	BRAWH3012662	0.000	41.917
10	BRAWH3021574	0.000	17.397
	BRAWH3022651	0.000	6.064
	BRAWH3037428	0.000	21.753
	BRCAN2019953	0.000	35.208
	BRCAN2022126	0.000	17.973
15	BRHIP3002000	10.458	0.000
	BRHIP3002691	0.000	30.700
	BRHIP3012997	0.000	3.431
	BRHIP3020046	0.000	3.749
	BRSTN2012069	0.429	0.140
20	BRSTN2016992	0.000	1.822
	BRTHA3010212	0.000	20.450
	CTONG2006235	0.000	6.064
	KIDNE2004531	80.699	0.000
	KIDNE2010049	11.987	0.000
25	KIDNE2014496	100.000	0.000
	KIDNE2015987	100.000	0.000
	KIDNE2016464	100.000	0.000
	KIDNE2017153	83.085	0.000
	KIDNE2018268	100.000	0.000
30	NT2RI2015533	0.000	11.506
	NT2RP7007387	7.156	0.000
	OCBBF3004487	0.000	16.771
	PLACE6008315	0.000	5.154
	SYNOV4004210	0.000	3.496
35	TESTI2005112	67.827	0.000
	THYMU3001776	22.094	0.000

	THYMU3002887	0.000	2.887
	THYMU3029795	37.093	0.000
	THYMU3032867	44.871	0.000
	TKIDN2000319	0.000	78.393
5	TKIDN2003396	0.000	100.000
	TKIDN2010602	0.000	100.000
	TKIDN2011051	0.000	100.000
	TKIDN2011160	0.000	100.000

10

The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE), and normal liver (LIVER) showed the following genes whose expression levels differed between the two.

15

Table 15

	Clone ID	LIVER	TLIVE
20	BRAWH3022651	14.200	0.000
	BRCAN2020412	0.000	74.979
	BRSTN2012069	0.000	0.390
	BRTHA3003736	18.647	0.000
	CTONG2006235	14.200	0.000
25	LIVER2008465	57.368	0.000
	TEST14013474	0.000	7.104
	THYMU3002887	6.762	0.000
	THYMU3038158	53.382	0.000
	TLIVE2000142	0.000	100.000
30	TLIVE2001616	0.000	100.000
	TLIVE2007736	0.000	90.642
	TLIVE2008797	0.000	100.000
	TRACH3027229	93.931	0.000
	THYMU3046350	0.000	47.489
35	TLIVE2007192	0.000	100.000

The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG), and normal lung (HLUNG) showed the following genes whose expression levels differed between the two.

Table 16

	Clone ID	HLUNG	TLUNG
10	BRACE3036283	27.376	0.000
	BRAMY2031516	27.091	0.000
	BRSTN2011961	2.124	0.000
	BRSTN2012069	0.763	0.000
15	HLUNG2012600	100.000	0.000
	MESAN2009156	38.142	0.000
	NTONG2008483	2.930	0.000
	PROST2007444	4.011	0.000
	TESTI4003703	16.229	0.000
20	TESTI4005653	1.824	0.000
	TESTI4013474	3.790	0.000
	TESTI4029297	16.229	0.000
	THYMU3001776	11.622	0.000
	THYMU3033626	20.615	0.000
25	THYMU3034671	8.747	0.000
	THYMU3041428	0.935	0.000
	TRACH3022198	30.484	0.000

30 The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER), and normal ovary (NOVER) showed the following genes whose expression levels differed between the two.

Table 17

	Clone ID	NOVAR	TOVAR
5	BRSTN2012069	5.861	6.386
	NOVAR2000783	90.145	0.000
	THYMU3002887	0.000	16.991

10 The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed the following genes whose expression levels differed between the two.

15 Table 18

	Clone ID	STOMA	TSTOM
	BRSTN2012069	1.995	4.062
20	CHONS2002829	11.118	0.000
	STOMA2003894	100.000	0.000
	STOMA2004663	47.516	0.000
	THYMU3001776	21.564	0.000
	TSTOM2000235	0.000	95.465
25	TSTOM2001571	0.000	100.000
	TSTOM2002611	0.000	100.000
	TSTOM2002682	0.000	100.000

30 The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed the following genes whose expression levels differed between the two.

Table 19

	Clone ID	UTERU	TUTER
5	BRACE2012528	0.566	0.000
	BRACE2017397	11.252	0.000
	BRACE3004371	4.481	0.000
	BRACE3036283	8.902	0.000
	BRACE3040863	21.335	0.000
10	BRAMY2031516	8.809	0.000
	BRAMY3005184	26.725	0.000
	BRAWH2004078	6.285	0.000
	BRAWH3004350	19.774	0.000
	BRAWH3022651	1.954	0.000
15	BRAWH3024186	11.902	0.000
	BRAWH3029806	10.629	0.000
	BRAWH3031342	6.474	0.000
	BRCAN2022126	5.791	0.000
	BRHIP3001076	53.896	0.000
20	BRHIP3002000	0.894	0.000
	BRHIP3002141	18.713	0.000
	BRHIP3005307	53.896	0.000
	BRHIP3007223	2.405	0.000
	BRHIP3017855	27.401	0.000
25	BRHIP3020046	1.208	0.000
	BRSTN2010089	7.869	0.000
	BRSTN2011961	0.345	0.000
	BRSTN2012069	0.271	3.583
	BRSTN2016892	3.559	0.000
30	BRTHA3003736	5.131	0.000
	BRTHA3011265	10.176	0.000
	BRTHA3023403	26.579	0.000
	BRTHA3027879	51.819	0.000
	CHONS2002829	11.691	0.000
35	CTONG2001932	12.322	0.000
	CTONG2003517	13.371	0.000

	CTONG2006235	1.954	0.000
	CTONG2011801	3.532	0.000
	CTONG3002518	10.064	0.000
	DFNES2001829	11.006	0.000
5	KIDNE2010049	4.101	76.623
	LIVER2008465	7.893	0.000
	NT2RI3005923	23.249	0.000
	OCBBF3001333	3.832	0.000
	OCBBF3004487	5.404	0.000
10	PLACE6008315	1.661	0.000
	PLACE7006240	30.024	0.000
	PROST2007444	5.217	0.000
	SPLEN2012571	3.792	0.000
	SYNOV4000598	35.608	0.000
15	SYNOV4009575	5.715	0.000
	T1ESE2000904	2.754	0.000
	TESTI4002072	3.983	0.000
	TESTI4002195	15.959	0.000
	TESTI4002774	9.787	0.000
20	TESTI4002799	1.053	9.842
	TESTI4003703	5.277	0.000
	TESTI4003944	41.606	0.000
	TESTI4005399	9.300	0.000
	TESTI4005653	1.779	0.000
25	TESTI4024245	40.205	0.000
	TESTI4029297	5.277	0.000
	THYMU3002887	0.930	0.000
	THYMU3021586	4.926	0.000
	THYMU3026350	17.045	0.000
30	THYMU3032798	2.306	0.000
	THYMU3034616	58.853	0.000
	THYMU3034671	19.911	0.000
	TRACH3003872	9.820	0.000
	TRACH3005699	22.893	0.000
35	TRACH3006800	34.742	0.000
	TRACH3008632	20.157	0.000

	TRACH3009008	5.843	0.000
	TUTER1000014	0.000	100.000
	TUTER2001433	0.000	100.000
	UTERU2000300	11.765	0.000
5	UTERU2014998	100.000	0.000
	UTERU2016464	100.000	0.000
	UTERU2016669	9.848	0.000
	UTERU2020226	78.491	0.000
	UTERU2022955	100.000	0.000
10	UTERU2023941	100.000	0.000
	UTERU2024042	100.000	0.000
	UTERU2027369	39.231	0.000
	UTERU2028377	100.000	0.000
	UTERU2029660	100.000	0.000
15	UTERU2035926	100.000	0.000
	UTERU2037423	100.000	0.000
	UTERU3000670	83.447	0.000
	UTERU3001029	100.000	0.000
	UTERU3001394	100.000	0.000
20	UTERU3001946	34.742	0.000
	UTERU3004635	100.000	0.000
	UTERU3005264	100.000	0.000
	UTERU3005422	25.298	0.000
	UTERU3006538	100.000	0.000
25	UTERU3006720	100.000	0.000
	UTERU3007108	100.000	0.000
	UTERU3009775	100.000	0.000
	UTERU3010029	100.000	0.000
	UTERU3010409	53.665	0.000
30	UTERU3010604	40.126	0.000
	UTERU3010892	100.000	0.000
	UTERU3010919	100.000	0.000
	UTERU3011092	100.000	0.000
	UTERU3011398	100.000	0.000
35	UTERU3011558	100.000	0.000
	UTERU3011579	34.742	0.000

	UTERU3011837	100.000	0.000
	UTERU3012293	100.000	0.000
	UTERU3012414	51.819	0.000
	UTERU3012476	100.000	0.000
5	UTERU3012599	100.000	0.000
	UTERU3012999	100.000	0.000
	UTERU3013167	54.394	0.000
	UTERU3013302	58.853	0.000
	UTERU3014274	100.000	0.000
10	UTERU3014647	100.000	0.000
	UTERU3014906	100.000	0.000
	UTERU3015011	16.834	0.000
	UTERU3015299	100.000	0.000
	UTERU3015647	100.000	0.000
15	UTERU3015844	100.000	0.000
	UTERU3016070	100.000	0.000
	UTERU3016273	53.896	0.000
	UTERU3016274	100.000	0.000
	UTERU3016308	100.000	0.000
20	UTERU3017441	100.000	0.000
	UTERU3017626	100.000	0.000
	UTERU3017995	13.044	0.000
	UTERU3018172	38.038	0.000
	UTERU3018255	100.000	0.000
25	UTERU2017492	5.197	0.000
	UTERU2025415	100.000	0.000
	UTERU2036507	100.000	0.000

30 The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed the following genes whose expression levels differed between the two.

Table 20

	Clone ID	NTONG	CTONG
5	BRACE2012528	0.000	0.883
	BRAMY4001863	0.000	55.803
	BRAWH3021574	0.000	17.507
	BRAWH3022651	0.000	3.051
	BRAWH3024186	0.000	18.588
10	BRHIP2027077	0.000	3.762
	BRHIP3001573	0.000	15.195
	BRHIP3002000	0.000	12.571
	BRHIP3007223	14.859	3.755
	BRHIP3012997	0.000	1.726
15	BRHIP3020046	0.000	3.773
	BRSSN2013696	0.000	6.652
	BRSTN2011961	2.134	0.539
	BRSTN2012069	0.000	0.018
	BRTHA2027229	0.000	3.410
20	BRTHA2033155	0.000	7.921
	BRTHA3011194	0.000	6.583
	BRTHA3022641	0.000	32.949
	CTONG2001932	0.000	38.485
	CTONG2003517	0.000	20.880
25	CTONG2006235	0.000	3.051
	CTONG2008989	0.000	100.000
	CTONG2009033	0.000	47.970
	CTONG2009570	0.000	100.000
	CTONG2010330	0.000	100.000
30	CTONG2011801	0.000	5.515
	CTONG2012123	0.000	100.000
	CTONG2014206	0.000	100.000
	CTONG2014959	0.000	100.000
	CTONG2020582	0.000	21.442
35	CTONG2026987	0.000	100.000
	CTONG2027150	0.000	100.000

	CTONG2027591	0.000	100.000
	CTONG2027783	0.000	100.000
	CTONG2027959	0.000	72.408
	CTONG3001605	0.000	100.000
5	CTONG3002518	0.000	15.716
	CTONG3002588	0.000	100.000
	CTONG3003669	0.000	100.000
	CTONG3008223	0.000	100.000
	NT2RI2009233	0.000	8.402
10	NTONG2002278	100.000	0.000
	NTONG2003805	100.000	0.000
	NTONG2004829	100.000	0.000
	NTONG2008483	17.664	2.976
	NTONG2009468	69.996	0.000
15	OCBBF3004487	0.000	8.439
	PLACE6008315	10.262	0.000
	PLACE7004103	9.531	12.044
	SKNMC2003639	0.000	19.285
	SPLEN2012571	0.000	5.921
20	SPLEN2019092	0.000	51.706
	SYNOV4009575	0.000	8.924
	T1ESE2000904	0.000	4.300
	TESTI2005564	0.000	6.821
	TESTI2018867	20.987	0.000
25	TESTI4002799	0.000	1.645
	TESTI4005653	0.000	7.408
	TESTI4032913	59.736	0.000
	THYMU3021586	0.000	7.693
	THYMU3047115	57.541	0.000
30	TRACH3006717	0.000	13.669
	TRACH3007625	0.000	4.379
	TRACH3016805	0.000	8.386
	TRACH3036932	0.000	27.304
	TRACH3038399	0.000	23.161
35	UTERU2000300	0.000	9.187
	CTONG2002832	0.000	20.880

CTONG2003764 0.000 24.325

5 The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA, or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN, or BRTHA) showed the following genes whose expression levels differed between the two.

	FCBBF	FEBRA	OGBBF	BRACE	BRALZ	BRAWY	BRAWH	BRCAN	BRCCG	BRHIP	BRSSN	BRSTN	BRTHA
	28.772	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	17.271
	0.000	0.000	0.000	0.000	0.000	0.000	14.497	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	8.220
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	3.670	18.684	5.210	0.000	15.817	12.212	5.275	0.000	6.215	1.911
	0.000	0.000	0.000	9.684	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	9.658	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.876	5.911	3.535	15.820	1.714	10.512	3.794	7.616	0.000	4.354	0.000	6.840	13.673
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	58.183	0.000	0.000	0.000	0.000	0.000	41.817	0.000	0.000	0.000
	0.000	0.000	0.000	3.348	0.000	2.376	0.000	0.000	0.000	4.813	0.000	0.000	0.000
	0.000	0.000	0.000	29.179	0.000	15.534	0.000	11.790	0.000	5.243	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	74.228	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	25.772
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		

BRHIP2015153	0.000	14.222	0.000	10.095	20.038	0.000	0.000	0.000	20.443	0.000	0.000	0.000
BRHIP2016125	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2017714	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2020930	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2021929	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2023735	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2024941	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2026346	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2027077	3.732	0.000	0.000	2.035	2.020	0.000	0.000	0.000	2.061	0.000	0.000	0.000
BRHIP2027563	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2029529	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP2029643	0.000	18.557	10.603	0.000	0.000	0.000	0.000	0.000	15.240	55.599	0.000	0.000
BRHIP2029663	0.000	54.907	0.000	0.000	0.000	0.000	0.000	0.000	45.093	0.000	0.000	0.000
BRHIP3000626	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3000859	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3001076	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	46.104	0.000	0.000	0.000
BRHIP3001141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3001338	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3001360	0.000	0.000	41.027	0.000	0.000	0.000	0.000	0.000	58.973	0.000	0.000	0.000
BRHIP3001481	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	38.435	0.000	0.000	0.000
BRHIP3001573	0.000	0.000	0.000	8.220	24.474	0.000	0.000	0.000	24.970	0.000	0.000	27.141
BRHIP3001878	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3002000	0.000	1.870	0.532	0.756	4.500	0.000	0.000	2.657	3.826	5.583	5.408	0.832
BRHIP3002114	0.000	0.000	27.684	0.000	0.000	0.000	0.000	0.000	39.793	0.000	0.000	0.000
BRHIP3002124	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3002141	0.000	39.113	0.000	0.000	0.000	0.000	0.000	0.000	16.008	0.000	0.000	0.000
BRHIP3002363	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3002691	15.322	0.000	10.303	8.357	0.000	0.000	0.000	0.000	16.923	0.000	0.000	18.395
BRHIP3002920	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	64.789	0.000	0.000	35.211
BRHIP3002931	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3003063	0.000	0.000	0.000	33.130	10.960	0.000	0.000	0.000	55.910	0.000	0.000	0.000
BRHIP3003126	0.000	0.000	25.807	0.000	0.000	0.000	0.000	0.000	74.193	0.000	0.000	0.000
BRHIP3003306	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.949	0.000	0.000	0.000
BRHIP3003340	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3003395	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3003688	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3003795	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	45.093	0.000	0.000	0.000
BRHIP3003845	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	10.774	0.000	0.000	0.000
BRHIP3003961	0.000	0.000	13.462	0.000	0.000	0.000	0.000	0.000	19.351	0.000	0.000	21.034
BRHIP3003984	0.000	0.000	29.254	0.000	0.000	0.000	0.000	0.000	28.033	0.000	0.000	15.236
BRHIP3004215	0.000	0.000	9.636	13.679	0.000	0.000	0.000	0.000	13.851	0.000	0.000	15.055
BRHIP3004710	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3004725	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3004774	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.480	0.000	0.000	0.000
BRHIP3004786	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3005037	0.000	0.000	0.000	0.000	39.520	0.000	0.000	0.000	82.401	0.000	0.000	0.000
BRHIP3005142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.949	0.000	0.000	0.000
BRHIP3005231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHIP3005307	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	46.104	0.000	0.000	0.000
BRHIP3005673	0.000	0.000	0.000	25.956	0.000	0.000	0.000	0.000	52.564	0.000	0.000	0.000
BRHIP3005801	0.000	0.000	13.302	0.000	0.000	0.000	0.000	0.000	19.121	0.000	67.577	0.000

BRHI P3021019	14.308	19.306	28.863	0.000	0.000	7.803	7.745	0.000	0.000	0.000	7.901	0.000	0.000	0.000	0.000
BRHI P3021499	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3021987	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	36.438	0.000	0.000	0.000	0.000
BRHI P3022656	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3023922	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3024703	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3024820	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3025795	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3025844	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3026231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3026551	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3027160	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3027191	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3027651	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3027947	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3028246	0.000	0.000	0.000	0.000	0.000	22.315	22.147	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRHI P3028570	0.000	0.000	0.000	0.000	0.000	0.000	31.957	0.000	0.000	0.000	22.595	0.000	0.000	0.000	0.000
BRHI P3028742	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	32.604	0.000	0.000	0.000	35.439
BRSSN2004303	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRSSN2004710	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRSSN2008464	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000
BRSSN2011843	22.111	0.000	14.868	8.495	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSSN2012157	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSSN2012198	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSSN2013696	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSSN2015497	0.000	0.000	0.000	12.675	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSSN2018218	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	7.931
BRSTN2000312	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2006466	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2006638	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2008475	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2009247	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2010089	0.000	16.447	0.000	4.683	0.000	0.000	6.598	0.000	23.372	0.000	0.000	0.000	0.000	23.789	0.000
BRSTN2010416	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2011688	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2011961	0.000	0.722	0.000	3.083	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2012089	0.157	0.401	0.047	0.517	0.718	0.029	0.047	0.000	1.026	0.000	0.000	0.000	0.000	1.044	1.285
BRSTN2016892	0.000	7.439	0.000	0.000	0.000	0.000	0.000	0.391	0.101	0.000	0.000	0.000	0.000	0.853	0.000
BRSTN2016918	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	10.759	0.000
BRSTN2016992	0.000	0.000	0.611	5.588	0.000	0.000	1.476	3.387	1.743	0.000	2.510	5.495	15.970	15.970	1.091
BRSTN2017104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	8.946	0.000	0.000	0.000	7.257	7.030	7.030	0.000
BRSTN2017151	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRSTN2018712	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRTHA2000969	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRTHA2001304	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000
BRTHA2001953	0.000	0.000	11.892	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000
BRTHA2002091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	9.786	0.000	0.000	0.000	10.615
BRTHA2003759	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000
BRTHA2005448	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000
BRTHA2006720	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000
BRTHA2008502	0.000	53.934	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	22.073	0.000	0.000	0.000	23.993

NT2R12009233	4.167	0.000	5.604	1.601	0.000	4.545	6.767	5.175	7.991	0.000	0.000	8.133	2.501
NT2R12010795	0.000	0.000	0.000	0.000	0.000	16.619	0.000	0.000	0.000	16.827	0.000	0.000	36.581
NT2R12015533	5.742	0.000	3.861	3.309	5.616	12.527	6.216	7.131	0.000	1.586	0.000	5.604	12.064
NT2R13005923	0.000	0.000	0.000	0.000	0.000	0.000	19.493	0.000	0.000	0.000	0.000	0.000	0.000
NT2R13009524	0.000	0.000	0.000	0.000	0.000	0.000	35.496	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP7007387	7.584	5.117	5.100	0.000	0.000	0.000	6.158	4.709	0.000	2.094	0.000	0.000	2.276
NT2RP8001604	0.000	17.297	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP8001605	0.000	0.000	0.000	0.000	0.000	0.000	29.324	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP8007920	10.963	0.000	31.946	1.404	0.000	0.000	1.978	0.000	0.000	0.000	7.363	0.000	0.000
NT2RP8009119	0.000	0.000	0.000	3.276	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NTONG2008483	1.476	1.992	1.985	0.000	0.000	0.000	2.397	1.833	5.661	0.815	0.000	5.761	1.772
NTONG2009468	0.000	0.000	0.000	13.482	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2000831	17.790	0.000	47.849	0.000	0.000	9.702	0.000	0.000	0.000	9.824	0.000	0.000	0.000
OCBBF2003518	0.000	2.570	1.281	0.000	0.000	1.039	2.082	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2004478	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2007039	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2009536	0.000	0.000	52.835	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2014745	0.000	0.000	63.640	36.360	0.000	0.000	0.000	0.000	0.000	0.000	0.000	47.165	0.000
OCBBF2016928	5.059	0.000	13.608	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2018229	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2018618	0.000	0.000	40.294	0.000	0.000	16.341	16.218	0.000	0.000	16.546	0.000	0.000	0.000
OCBBF2019761	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2024589	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2024779	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2025631	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2030927	0.000	0.000	55.216	0.000	0.000	44.784	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2036019	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3000743	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3000830	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001076	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001202	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001333	0.000	0.000	11.974	4.561	0.000	6.475	9.639	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001616	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3003745	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3004487	0.000	0.000	11.257	6.432	0.000	4.565	4.531	0.000	0.000	4.522	0.000	0.000	0.000
OCBBF3004908	0.000	47.686	11.882	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3005330	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3005843	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3006986	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3007078	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3007704	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3008392	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3008835	0.000	0.000	52.835	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3009244	0.000	0.000	42.785	0.000	0.000	34.702	0.000	0.000	0.000	0.000	0.000	47.165	0.000
PLAGE5000492	0.000	0.000	0.000	0.000	0.000	0.000	0.000	56.315	0.000	0.000	0.000	0.000	0.000
PLAGE6003004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	38.390	0.000
PLAGE6008315	0.000	0.000	1.730	0.000	0.000	1.403	0.000	0.000	4.933	0.000	0.000	5.021	0.000
PLAGE6010936	0.000	0.000	0.000	0.000	0.000	12.399	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PLAGE7004103	0.000	0.000	1.607	0.918	0.000	1.303	3.880	0.000	0.000	5.278	0.000	4.302	0.000
PLAGE7006240	0.000	0.000	0.000	0.000	0.000	0.000	25.174	0.000	0.000	0.000	0.000	0.000	0.000
PROST2007444	0.000	5.452	4.075	5.433	0.000	1.102	4.374	0.000	0.000	5.578	8.140	3.638	0.000

The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed the following genes whose expression levels differed between the two.

Table 22

Clone ID	HEART	FEHRT
BRACE2012528	6.328	0.000
BRACE3004371	25.063	0.000
BRCAN2003814	0.000	90.076
BRSTN2011961	1.932	0.000
BRSTN2012069	1.641	0.394
BRSTN2016992	6.566	0.000
HEART2002531	100.000	0.000
NTONG2008483	5.330	0.000
PROST2002078	16.213	0.000
TIESE2000609	15.163	0.000

The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed the following genes whose expression levels differed between the two.

Table 23

Clone ID	KIDNE	FEKID
BRACE3004371	13.097	0.000
BRAMY2039630	60.511	0.000
BRAMY3004364	23.683	0.000
BRAWH2004078	18.371	0.000
BRHIP3002000	10.458	0.000
BRSTN2011961	0.000	6.265

	BRSTN2012069	0.429	1.841
	BRTHA2027229	0.000	19.799
	KIDNE2004531	80.699	0.000
	KIDNE2010049	11.987	0.000
5	KIDNE2014496	100.000	0.000
	KIDNE2015987	100.000	0.000
	KIDNE2016464	100.000	0.000
	KIDNE2017153	83.085	0.000
	KIDNE2018268	100.000	0.000
10	NT2RP7007387	7.156	0.000
	TESTI2005112	67.827	0.000
	TESTI4002799	0.000	9.553
	THYMU3001776	22.094	0.000
	THYMU3029795	37.093	0.000
15	THYMU3032867	44.871	0.000

The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed the following genes whose expression levels differed between the two.

Table 24

	Clone ID	HLUNG	FELNG
	BRACE3036283	27.376	0.000
	BRAMY2031516	27.091	0.000
	BRSTN2011961	2.124	0.000
30	BRSTN2012069	0.763	2.238
	HLUNG2012600	100.000	0.000
	MESAN2009156	38.142	0.000
	NTONG2008483	2.930	0.000
	PROST2007444	4.011	0.000
35	TESTI4003703	16.229	0.000
	TESTI4005653	1.824	0.000

	TEST14013474	3.790	0.000
	TEST14029297	16.229	0.000
	THYMU3001776	11.622	0.000
	THYMU3033626	20.615	0.000
5	THYMU3034671	8.747	0.000
	THYMU3041428	0.935	0.000
	THYMU3044188	0.000	96.268
	TRACH3022198	30.484	0.000

10

EXAMPLE 9In-silico expression frequency analysis based on large-scale
analysis data for 5'-end sequences

15 Analyzing the expression level of a gene in various organs,
tissues or cells is an exceedingly important step in clarifying
the function of that organ, tissue, or cell, as well as in
clarifying gene networks and in studying a causative gene of a
morbid state. For example, if the expression level of a gene
differs between a normal tissue and a malignant tissue, there is
20 a possibility that that gene is involved in cancer. If tissue
canceration can be suppressed by downregulating the expression
of that gene, a compound comprising such downregulating activity
can be used as an anticancer drug.

25 Various methods for analyzing gene expression frequency
have been developed. For example, wet-type experiment-based
methods include Northern blotting and RT-PCR, and of the use of
gene chips and microarrays, where target samples synthesized
from tissue or cell-derived RNA are hybridized to
polynucleotides that comprise partial gene sequences synthesized
30 on a base, or cDNA clones attached as plasmids directly to a
base, and then signals are detected (Experiment Medicine, Vol.
17, No. 8, 980-1056 (1999), Eds., Muramatsu and Nawa, Cell
Technology, Suppl. "DNA Microarray and New PCR Methods"
(Shujunsha, 2000)). A method called "ATAC-PCR" is also
35 available (Kato. K (1997) Nucleic Acids Res. 25, 4694-6), which
comprises the steps of cleaving cDNA synthesized from tissue or

cell-derived RNA, attaching adapters of different length depending on the type of tissue or cell, carrying out competitive PCR using a primer which contains a fluorescent dye and a sequence complementary to the adapter, and a primer specific to the gene, and then analyzing the expression level of the gene. In addition, an in-silico analysis-based method using sequence data is available. A database called BODYMAP (<http://bodymap.ims.u-tokyo.ac.jp/>) has been constructed by randomly extracting gene clones from cDNA libraries of various tissues and cells, combining clones homologous to one another as a cluster, classifying the genes in each cluster unit based on homology information on the nucleotide sequences of cDNA 3' ends, and then obtaining information on gene expression frequency by comparing the number of clones in respective clusters.

Both experiment-based and in-silico analysis-based methods are widely accepted methods of gene expression analysis. These methods, and almost all other established methods for analyzing the frequency of gene expression, are based on analysis of 3'-end gene sequences. In human genes the 3'-untranslated regions (3'-UTR) are usually long, and thus there is controversy as to whether the results of such methods directly correspond to gene expression frequency and polypeptide expression pattern. However, the analysis method for gene expression frequency of the present invention is based on 5'-end gene sequences, and thus the expression pattern of each gene is a more accurate and faithful reproduction of the original *in vivo* pattern.

cDNA libraries in which the probability of cDNA completeness is exceedingly high were prepared from various tissues and cells as described in Example 1. cDNA clones were randomly selected from each library, the cDNA 5'-end sequences were determined, and a sequence database was constructed using this data. This database contains the nucleotide sequences of 1,402,069 clones, a sufficiently large population for analysis. The libraries used in the analysis, the number of cDNA clones whose 5'-end sequences were determined, and the weighted value

for a single sequence in each library (100 divided by the number of sequences analyzed in each library) are described below.

Table 25

5	<hr/>		
	Library Names	Number of clones whose 5' ends were analyzed	Weighted values for single sequences (100/Number of sequences)
<hr/>			
10	3NB69	8182	0.012221951
	ACTVT	684	0.14619883
	ADIPS	614	0.16286645
	ADRGL	10300	0.009708738
	AHMSC	671	0.149031297
15	ASTRO	17226	0.005805178
	BEAST	2736	0.036549708
	BGG11	1904	0.052521008
	BLADE	8503	0.011760555
	BNGH4	7739	0.012921566
20	BRACE	84087	0.001189244
	BRALZ	16517	0.006054368
	BRAMY	59232	0.001688277
	BRASW	158	0.632911392
	BRAWH	59682	0.001675547
25	BRCAN	26014	0.003844084
	BRCOC	16847	0.005935775
	BRHIP	58498	0.00170946
	BRSSN	16035	0.006236358
	BRSTN	16552	0.006041566
30	BRTHA	53818	0.001858114
	CD34C	1421	0.070372977
	CERVX	2888	0.034626039
	CHONS	2694	0.037119525
	COLON	8501	0.011763322
35	CORDB	711	0.140646976
	CTONG	32043	0.003120806

	D30ST	5112	0.019561815
	D60ST	889	0.112485939
	D90ST	4426	0.022593764
	DFNES	10126	0.009874593
5	ERLTF	2178	0.045913682
	FCBBF	32305	0.003095496
	FEBRA	23941	0.004176935
	FEHRT	2866	0.034891835
	FEKID	2759	0.036245016
10	FELIV	186	0.537634409
	FELNG	2775	0.036036036
	HCASM	8989	0.011124708
	HCHON	9432	0.010602205
	HEART	8946	0.01117818
15	HELAC	680	0.147058824
	HHDPC	8476	0.011798018
	HLUNG	16272	0.006145526
	HSYRA	7985	0.012523482
	IMR32	16914	0.005912262
20	JCMLC	2171	0.046061723
	KIDNE	17119	0.005841463
	LIVER	6885	0.014524328
	LYMPB	2630	0.038022814
	MAMGL	184	0.543478261
25	MESAN	16095	0.00621311
	MESTC	691	0.1447178
	N1ESE	2628	0.03805175
	NB9N4	1764	0.056689342
	NCRRM	703	0.142247511
30	NCRRP	699	0.143061516
	NESOP	2805	0.035650624
	NETRP	9236	0.010827198
	NHNPC	2392	0.04180602
	NOVAR	2504	0.039936102
35	NT2NE	16468	0.006072383
	NT2RI	32842	0.003044882

	NT2RM	2074	0.048216008
	NT2RP	24763	0.004038283
	NTISM	181	0.552486188
	NTONG	8098	0.012348728
5	OCBBF	48042	0.002081512
	PANCR	182	0.549450549
	PEBLM	7940	0.012594458
	PERIC	8860	0.011286682
	PLACE	33535	0.002981959
10	PROST	16829	0.005942124
	PUAEN	10577	0.009454477
	RECTM	2743	0.036456435
	SALGL	185	0.540540541
	SKMUS	8470	0.011806375
15	SKNMC	7656	0.013061651
	SKNSH	8692	0.011504832
	SMINT	16913	0.005912612
	SPLEN	34307	0.002914857
	STOMA	8770	0.011402509
20	SYNOV	27671	0.003613892
	T1ESE	2687	0.037216226
	TBAES	8484	0.011786893
	TCERX	2828	0.035360679
	TCOLN	2815	0.035523979
25	TESOP	8723	0.011463946
	TESTI	91301	0.001095278
	THYMU	71574	0.001397155
	TKIDN	16123	0.00620232
	TLIVE	8681	0.01151941
30	TLUNG	2884	0.034674064
	TOVAR	2740	0.03649635
	TRACH	53281	0.001876842
	TSTOM	2779	0.035984167
	TUTER	2678	0.037341299
35	UMVEN	633	0.157977883
	UTERU	50040	0.001998401

Using a nucleotide sequence homology search program, the nucleotide sequences of respective clones in this database were categorized (clustered) into groups, each of which contained homologous sequences. Cluster members (the number of clones whose 5' ends were analyzed) were totalized and normalized for each library, resulting in an abundance ratio of genes in the cDNA library. In addition, 17,547 genes, including full-length cDNAs of the present invention, were assigned to a cluster using a nucleotide sequence homology search program.

In addition to the abundance ratio of the assigned genes in cDNA libraries, the sums of the weighted values for single sequences in each library were also calculated. For example, the expression of the clone BRACE2000753 was detectable in the BRACE, SPLEN, and THYMU libraries, based on expression analysis results. The single-sequence weighted values for these libraries are 0.001189244, 0.002914857, and 0.001397155 respectively, as seen in Table 1. Thus, their sum is 0.005501257. This parameter serves as an index for gene expression frequency in entire libraries. The higher this value, the greater the gene expression level. Listed below are the clone names of the 17,176 genes assigned to clusters, the number of cDNA clones whose 5' end sequences were determined, and the sum of the weighted values for single sequences, cluster names, and the number of clones whose 5' ends were analyzed.

Table 26

Names of clones assigned to clusters	Sums of weighted values for single sequences	Cluster names	Number of clones constituting clusters
3NB691000018	0.018027129	76695	2
3NB691000085	0.019353319	56523	3
3NB691000113	0.024745432	48667	2

	3NB691000116	0. 103029787	73878	17
	3NB691000129	0. 066363755	74681	5
	3NB691000173	0. 212194846	38917	27
	3NB691000191	0. 02737028	77141	4
5	3NB692000012	0. 012221951	168462	1
	3NB692000029	0. 012221951	271188	1
	3NB692000102	0. 012221951	110443	1
	3NB692000154	0. 012221951	201888	1
	3NB692000276	0. 012221951	268979	1
10	3NB692000281	0. 761173312	35400	45
	3NB692000305	0. 012221951	265781	1
	3NB692000330	0. 379866613	53361	33
	3NB692000374	0. 154501611	57823	29
	3NB692000429	0. 012221951	249303	1
15	3NB692000484	0. 016398886	123962	2
	3NB692000529	0. 015026689	223096	3
	3NB692000545	0. 059391668	134996	14
	3NB692000912	0. 356619986	48215	43
	3NB692000973	0. 023726783	201722	2
20	3NB692001002	0. 085645793	67876	7
	3NB692001022	0. 134669151	41083	19
	3NB692001034	0. 012221951	221723	1
	3NB692001040	0. 012221951	115756	1
	3NB692001123	0. 012221951	266961	1
25	3NB692001267	0. 012221951	265274	1
	3NB692001288	0. 1118352	117265	23
	3NB692001334	0. 624221602	49741	81
	3NB692001339	0. 071442272	47481	4
	3NB692001349	0. 012221951	175232	1
30	3NB692001366	0. 013317229	3969	2
	3NB692001408	0. 012221951	126880	1
	3NB692001433	0. 048706104	130520	3
	3NB692001442	0. 138711778	127766	17
	3NB692001459	0. 029639045	200852	3
35	3NB692001471	0. 012221951	75788	1
	3NB692001496	0. 021768101	84831	5

	3NB692001501	0. 012221951	268316	1
	3NB692001507	0. 012221951	268061	1
	3NB692001511	0. 019462755	167015	3
	3NB692001519	0. 012221951	271957	1
5	3NB692001520	0. 013619106	104334	2
	3NB692001528	0. 071227801	139135	6
	3NB692001538	0. 084340651	122218	7
	3NB692001548	0. 012221951	96322	1
	3NB692001557	0. 027621147	91468	4
10	3NB692001637	0. 036967383	168210	3
	3NB692001719	0. 024327187	94876	6
	3NB692001853	0. 063988222	34169	5
	3NB692001861	0. 012221951	193198	1
	3NB692002051	0. 019613515	178660	3
15	3NB692002365	0. 012221951	4137	1
	3NB692002685	0. 012221951	217529	1
	3NB692002806	0. 012221951	154266	1
	3NB692003538	0. 012221951	208889	1
	3NB692004045	0. 012221951	284307	1
20	3NB692004724	0. 012221951	196462	1
	3NB692005439	0. 012221951	185399	1
	3NB692006952	0. 028620836	68822	3
	3NB692008178	0. 013317229	46324	2
	3NB692008729	0. 012221951	135639	1
25	ACTVT2000380	0. 14619883	240854	1
	ADIPS1000064	0. 16286645	41464	1
	ADIPS2000069	0. 16286645	278077	1
	ADIPS2000088	0. 325732899	273369	2
	ADIPS2000245	0. 16286645	260321	1
30	ADIPS2000425	0. 215847182	124522	9
	ADRGL1000002	0. 101756095	64755	44
	ADRGL1000018	0. 034647887	46754	15
	ADRGL1000033	0. 043883526	34724	5
	ADRGL1000038	0. 009708738	66512	1
35	ADRGL1000065	0. 02971239	34887	11
	ADRGL1000067	0. 009708738	8956	1

	ADRGL1000111	0.011105893	55238	2
	ADRGL1000144	0.05013397	52060	8
	ADRGL1000147	0.019417476	53719	2
	ADRGL1000160	0.077669903	10013	8
5	ADRGL1000165	0.009708738	73605	1
	ADRGL1000182	0.009708738	65035	1
	ADRGL2000006	0.161178621	129178	41
	ADRGL2000042	0.065977455	94764	17
	ADRGL2000056	0.011105893	208582	2
10	ADRGL2000064	0.009708738	184566	1
	ADRGL2000074	0.011397014	157554	2
	ADRGL2000085	0.009708738	184572	1
	ADRGL2000097	0.075366581	171199	10
	ADRGL2000117	0.019631485	114323	4
15	ADRGL2000142	0.009708738	141891	1
	ADRGL2000172	0.009708738	182717	1
	ADRGL2000248	0.009708738	223982	1
	ADRGL2000261	0.009708738	207317	1
	ADRGL2000323	0.012623595	236322	2
20	ADRGL2000328	0.024889644	175865	6
	ADRGL2000353	0.009708738	215172	1
	ADRGL2000384	0.067961165	12648	7
	ADRGL2000428	0.009708738	234148	1
	ADRGL2000636	0.009708738	75522	1
25	ADRGL2000644	0.015763106	214709	2
	ADRGL2000968	0.009708738	196722	1
	ADRGL2001119	0.009708738	112417	1
	ADRGL2001229	0.009708738	215864	1
	ADRGL2001287	0.009708738	197023	1
30	ADRGL2001301	0.009708738	241888	1
	ADRGL2001352	0.019587871	192434	4
	ADRGL2001354	0.009708738	223064	1
	ADRGL2001554	0.009708738	224065	1
	ADRGL2001651	0.009708738	222162	1
35	ADRGL2001756	0.009708738	85903	1
	ADRGL2001830	0.014018789	65424	3

	ADRGL2001836	0. 009708738	245756	1
	ADRGL2001854	0. 009708738	243277	1
	ADRGL2002013	0. 018625967	119719	7
	ADRGL2002029	0. 009708738	78836	1
5	ADRGL2002191	0. 013106475	63260	3
	ADRGL2002260	0. 011105893	188977	2
	ADRGL2002392	0. 009708738	94613	1
	ADRGL2002477	0. 098491284	97270	26
	ADRGL2002679	0. 013465797	130441	3
10	ADRGL2002753	0. 019417476	231793	2
	ADRGL2002857	0. 009708738	127516	1
	ADRGL2003017	0. 009708738	46472	1
	ADRGL2003329	0. 009708738	152935	1
	ADRGL2003552	0. 009708738	283156	1
15	ADRGL2003585	0. 009708738	15181	1
	ADRGL2003638	0. 009708738	134901	1
	ADRGL2003684	0. 009708738	155321	1
	ADRGL2003773	0. 009708738	223161	1
	ADRGL2003785	0. 011418198	69967	2
20	ADRGL2004031	0. 009708738	164853	1
	ADRGL2004077	0. 009708738	22835	1
	ADRGL2004451	0. 019417476	72403	2
	ADRGL2004459	0. 019417476	189693	2
	ADRGL2004676	0. 038439333	112371	8
25	ADRGL2004708	0. 009708738	163374	1
	ADRGL2004724	0. 009708738	174384	1
	ADRGL2004749	0. 009708738	192682	1
	ADRGL2004770	0. 009708738	200652	1
	ADRGL2004777	0. 009708738	131595	1
30	ADRGL2004833	0. 009708738	80679	1
	ADRGL2005336	0. 009708738	17560	1
	ADRGL2005564	0. 009708738	24035	1
	ADRGL2005756	0. 009708738	187567	1
	ADRGL2005838	0. 015854264	5613	2
35	ADRGL2005926	0. 038834951	145927	4
	ADRGL2005961	0. 009708738	3196	1

	ADRGL2006034	0. 009708738	101275	1
	ADRGL2006124	0. 009708738	32168	1
	ADRGL2006177	0. 009708738	149214	1
	ADRGL2006193	0. 009708738	146749	1
5	ADRGL2006233	0. 016534781	47690	3
	ADRGL2006377	0. 009708738	77853	1
	ADRGL2006677	0. 009708738	186902	1
	ADRGL2006732	0. 009708738	101903	1
	ADRGL2006767	0. 009708738	275340	1
10	ADRGL2006817	0. 009708738	213653	1
	ADRGL2006846	0. 009708738	187510	1
	ADRGL2006886	0. 009708738	176480	1
	ADRGL2007080	0. 009708738	190702	1
	ADRGL2007125	0. 009708738	45966	1
15	ADRGL2007283	0. 009708738	167805	1
	ADRGL2007313	0. 017100302	168347	3
	ADRGL2007357	0. 009708738	186500	1
	ADRGL2007636	0. 009708738	155823	1
	ADRGL2007651	0. 009708738	144684	1
20	ADRGL2007810	0. 009708738	99151	1
	ADRGL2007877	0. 009708738	197625	1
	ADRGL2007906	0. 018592193	81944	5
	ADRGL2007974	0. 011397014	174372	2
	ADRGL2008023	0. 009708738	122769	1
25	ADRGL2008331	0. 009708738	223423	1
	ADRGL2008337	0. 009708738	261136	1
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	BRACE2000183	0. 036549923	167435	2
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	BRACE2000232	0. 001189244	204443	1
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	BRACE2000256	0. 001189244	207459	1
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30	BRACE2000267	0. 012536959	102199	5
	BRACE2000280	0. 008940271	112431	3
	BRACE2000300	0. 031521611	95671	11
	BRACE2000307	0. 142252985	132485	49
	BRACE2000331	0. 002864792	18972	2
35	BRACE2000332	0. 061728861	126335	12
	BRACE2000347	0. 064814986	182381	17

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5	BRACE2000441	0. 001189244	146945	1
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10	BRACE2000526	0. 001189244	216121	1
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15	BRACE2000577	0. 002284523	71681	2
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	BRACE2000965	0. 001189244	158015	1
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15	BRACE2001269	0. 001189244	230267	1
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35	BRACE2001534	0. 054321394	173923	6
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	BRACE2002202	0.004663012	181084	4
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	BRACE2002444	0.001189244	41749	1
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20	BRACE2002857	0.001189244	160288	1
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25	BRACE2002948	0.001189244	245402	1
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	BRACE2003431	0. 001189244	171176	1
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20	BRACE2006258	0.204556781	67510	34
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25	BRACE2006319	0.047792784	49721	19
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35	BRACE2007109	0. 17553833	108689	65
	BRACE2007138	0. 001189244	230550	1

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	BRACE2007174	0. 010725179	118448	5
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5	BRACE2007201	0. 002898705	247830	2
	BRACE2007203	0. 001189244	234245	1
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	BRACE2007262	0. 001189244	126993	1
10	BRACE2007274	0. 001189244	241721	1
	BRACE2007281	0. 001189244	99385	1
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25	BRACE2007538	0. 001189244	40271	1
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35	BRAMY2012555	0. 003376553	185592	2
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	BRAMY2012731	0.001688277	266298	1
5	BRAMY2012776	0.001688277	143687	1
	BRAMY2012880	0.003376553	113376	2
	BRAMY2012881	0.003546391	65904	2
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15	BRAMY2013621	0.00572656	182111	2
	BRAMY2013659	0.00576819	155141	3
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20	BRAMY2013944	0.001688277	181579	1
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	BRAMY2014019	0.001688277	177887	1
	BRAMY2014205	0.011694423	126460	4
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25	BRAMY2014462	0.003397737	108055	2
	BRAMY2014469	0.003376553	145453	2
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30	BRAMY2015211	0.012899034	152308	4
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	BRAMY2015503	0.001688277	92331	1
35	BRAMY2015516	0.001688277	279553	1
	BRAMY2015550	0.004943546	163106	3

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5	BRAMY2015782	0. 042787761	206855	4
	BRAMY2015833	0. 036348251	109722	12
	BRAMY2015855	0. 002877521	148057	2
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	BRAMY2016611	0. 261569543	75529	133
20	BRAMY2016706	0. 033805049	173354	6
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25	BRAMY2017014	0. 001688277	150224	1
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	BRAMY2018122	0. 013207687	17774	2
35	BRAMY2018126	0. 001688277	30015	1
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5	BRAMY2018396	0.001688277	181631	1
	BRAMY2018467	0.001688277	39335	1
	BRAMY2018635	0.006168562	124266	4
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	BRAMY2019600	0.020752286	149067	9
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30	BRAMY2020427	0.282979705	33258	37
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5	BRAMY2021142	0. 006257322	133382	5
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10	BRAMY2021523	0. 007901386	202729	2
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	BRAMY2021746	0. 001688277	4424	1
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	BRAMY2022301	0. 001688277	239395	1
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25	BRAMY2022445	0. 003565118	176556	2
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30	BRAMY2022723	0. 004735635	196520	3
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	BRAMY2022796	0. 001688277	197503	1
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35	BRAMY2022984	0. 001688277	145187	1
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15	BRAMY2044838	0.005404505	252610	3
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25	BRAMY2046742	0.001688277	195740	1
	BRAMY2046871	0.0050521	213129	3
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30	BRAMY2047280	0.001688277	179986	1
	BRAMY2047420	0.165408115	117426	10
	BRAMY2047676	0.001688277	170182	1
	BRAMY2047692	0.001688277	150911	1
	BRAMY2047746	0.001688277	160869	1
35	BRAMY2047751	0.001688277	240602	1
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	BRAMY2047884	0. 001688277	145301	1
	BRAMY2047948	0. 001688277	260960	1
	BRAMY3000206	0. 001688277	191074	1
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5	BRAMY3000213	0. 001688277	208662	1
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	BRAMY3000307	0. 001688277	14805	1
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10	BRAMY3001356	0. 001688277	240026	1
	BRAMY3001401	0. 001688277	282047	1
	BRAMY3001409	0. 001688277	122846	1
	BRAMY3001794	0. 001688277	278756	1
	BRAMY3002120	0. 003085432	274920	2
15	BRAMY3002312	0. 001688277	212407	1
	BRAMY3002329	0. 024733489	88376	15
	BRAMY3002458	0. 013496638	50360	8
	BRAMY3002508	0. 001688277	187663	1
	BRAMY3002620	0. 002877521	263532	2
20	BRAMY3002803	0. 011613011	6275	6
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	BRAMY3002886	0. 001688277	283709	1
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	BRAMY3003026	0. 003769789	171950	2
25	BRAMY3003109	0. 001688277	235868	1
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	BRAMY3003310	0. 003085432	29786	2
	BRAMY3003566	0. 001688277	1038	1
	BRAMY3003723	0. 001688277	273171	1
30	BRAMY3003935	0. 01069797	109078	7
	BRAMY3004126	0. 003363824	269938	2
	BRAMY3004224	0. 005073284	90383	3
	BRAMY3004364	0. 024665517	167502	7
	BRAMY3004377	0. 202027897	108797	44
35	BRAMY3004672	0. 001688277	198821	1
	BRAMY3004800	0. 022011049	46315	13

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	BRAMY3005091	0. 008730003	70985	4
	BRAMY3005184	0. 00747765	83059	4
5	BRAMY3005656	0. 001688277	260511	1
	BRAMY3005912	0. 007823825	177921	5
	BRAMY3005932	0. 002877521	82603	2
	BRAMY3006032	0. 001688277	186399	1
	BRAMY3006297	0. 001688277	253799	1
10	BRAMY3006761	0. 015262219	60379	9
	BRAMY3007078	0. 003397737	211502	2
	BRAMY3007206	0. 001688277	283003	1
	BRAMY3007311	0. 021327119	144415	9
	BRAMY3007350	0. 001688277	27494	1
15	BRAMY3007449	0. 001688277	266907	1
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	BRAMY3007609	0. 001688277	256744	1
	BRAMY3007723	0. 001688277	257850	1
	BRAMY3007968	0. 001688277	138565	1
20	BRAMY3008044	0. 093406814	60946	38
	BRAMY3008088	0. 001688277	277370	1
	BRAMY3008096	0. 002877521	128660	2
	BRAMY3008335	0. 009432945	77458	5
	BRAMY3008436	0. 119621588	6885	51
25	BRAMY3008466	0. 001688277	249700	1
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	BRAMY3008650	0. 001688277	255619	1
	BRAMY3008937	0. 001688277	265634	1
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30	BRAMY3009207	0. 001688277	260172	1
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	BRAMY3009782	0. 003546391	185685	2
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35	BRAMY3009904	0. 001688277	259738	1
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	BRAMY3010264	0. 003363824	234713	2
	BRAMY3010321	0. 001688277	232211	1
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5	BRAMY3010603	0. 001688277	220417	1
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	BRAMY4000089	0. 032925039	111406	17
	BRAMY4000095	0. 011468135	70851	3
	BRAMY4000229	0. 004735635	261921	3
10	BRAMY4000277	0. 001688277	260995	1
	BRAMY4000915	0. 003397737	122639	2
	BRAMY4000962	0. 001688277	283461	1
	BRAMY4001173	0. 001688277	210285	1
	BRAMY4001200	0. 001688277	201028	1
15	BRAMY4001234	0. 003085432	177802	2
	BRAMY4001449	0. 001688277	221870	1
	BRAMY4001652	0. 001688277	210095	1
	BRAMY4001863	0. 011185159	109043	5
	BRAMY4001913	0. 001688277	125997	1
20	BRAMY4002575	0. 001688277	238638	1
	BRAMY4002628	0. 023589801	141596	11
	BRASW1000053	0. 632911392	218746	1
	BRASW1000125	0. 638952958	187197	2
	BRAWH1000001	0. 050352377	61329	21
25	BRAWH1000002	0. 001675547	66770	1
	BRAWH1000007	0. 018646974	6612	5
	BRAWH1000037	0. 091889673	54702	24
	BRAWH1000040	0. 24351653	11924	49
	BRAWH1000045	0. 167388547	79272	64
30	BRAWH1000083	0. 036981447	9715	10
	BRAWH1000093	0. 36328603	48128	52
	BRAWH1000094	0. 039797585	39402	14
	BRAWH1000116	0. 001675547	43181	1
	BRAWH1000127	0. 052416584	37367	19
35	BRAWH1000130	0. 001675547	67297	1
	BRAWH1000157	0. 001675547	64749	1

	BRAWH1000162	0. 091810869	30660	32
	BRAWH1000164	0. 001675547	75232	1
	BRAWH1000167	0. 092619948	51003	33
	BRAWH1000168	0. 001675547	128265	1
5	BRAWH1000174	0. 058484446	75043	25
	BRAWH1000180	0. 001675547	40597	1
	BRAWH1000369	0. 001675547	165088	1
	BRAWH2000034	0. 001675547	273204	1
	BRAWH2000048	0. 001675547	259623	1
10	BRAWH2000071	0. 001675547	69516	1
	BRAWH2000082	0. 436810495	55088	158
	BRAWH2000093	0. 001675547	228500	1
	BRAWH2000109	0. 001675547	136811	1
	BRAWH2000131	0. 007729915	206593	2
15	BRAWH2000142	0. 010996329	117660	4
	BRAWH2000169	0. 015895751	114160	3
	BRAWH2000177	0. 020956106	23588	7
	BRAWH2000218	0. 003533661	45764	2
	BRAWH2000232	0. 001675547	122780	1
20	BRAWH2000248	0. 001675547	169569	1
	BRAWH2000256	0. 001675547	245732	1
	BRAWH2000274	0. 08487909	126191	44
	BRAWH2000323	0. 001675547	106322	1
	BRAWH2000353	0. 002864792	87260	2
25	BRAWH2000370	0. 001675547	195714	1
	BRAWH2000409	0. 001675547	221617	1
	BRAWH2000417	0. 271182045	85514	92
	BRAWH2000443	0. 029573251	105194	11
	BRAWH2000460	0. 274541089	10111	76
30	BRAWH2000471	0. 001675547	267212	1
	BRAWH2000476	0. 006952582	93782	4
	BRAWH2000482	0. 110393093	13399	26
	BRAWH2000488	0. 016619307	133749	6
	BRAWH2000494	0. 018430826	140072	6
35	BRAWH2000500	0. 002864792	192393	2
	BRAWH2000503	0. 008076427	131331	4

	BRAWH2000522	0. 09244356	39525	18
	BRAWH2000554	0. 001675547	265277	1
	BRAWH2000588	0. 133555816	79239	29
	BRAWH2000595	0. 013436102	119870	2
5	BRAWH2000633	0. 126392578	31367	18
	BRAWH2000636	0. 317081402	80819	122
	BRAWH2000643	0. 001675547	231904	1
	BRAWH2000651	0. 001675547	144148	1
	BRAWH2000682	0. 001675547	95684	1
10	BRAWH2000686	0. 137074917	38929	51
	BRAWH2000697	0. 165643883	125094	44
	BRAWH2000752	0. 001675547	130443	1
	BRAWH2000839	0. 407966855	38528	119
	BRAWH2000859	0. 003552389	214221	2
15	BRAWH2000866	0. 001675547	255369	1
	BRAWH2000892	0. 001675547	219414	1
	BRAWH2000901	0. 001675547	280013	1
	BRAWH2000924	0. 583840525	60800	159
	BRAWH2000926	0. 039727297	109375	2
20	BRAWH2000944	0. 032118304	103162	11
	BRAWH2000984	0. 001675547	122613	1
	BRAWH2001019	0. 073467058	4310	21
	BRAWH2001037	0. 041779669	170115	15
	BRAWH2001052	0. 001675547	270537	1
25	BRAWH2001092	0. 953353157	65081	148
	BRAWH2001103	0. 025497494	217133	5
	BRAWH2001129	0. 003552389	143882	2
	BRAWH2001137	0. 001675547	178414	1
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30	BRAWH2001159	0. 001675547	80868	1
	BRAWH2001166	0. 05308009	96586	15
	BRAWH2001171	0. 271297828	45061	101
	BRAWH2001186	0. 058806701	67320	6
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35	BRAWH2001238	0. 013858127	121814	7
	BRAWH2001239	0. 022965193	151246	5

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	BRAWH2001321	0. 195185305	40551	78
	BRAWH2001355	0. 001675547	104096	1
	BRAWH2001378	0. 001675547	128073	1
5	BRAWH2001395	0. 398667125	6827	161
	BRAWH2001406	0. 049495121	106201	7
	BRAWH2001412	0. 011143487	197652	4
	BRAWH2001418	0. 064965414	99926	17
	BRAWH2001424	0. 0329093	72850	7
10	BRAWH2001436	0. 001675547	260418	1
	BRAWH2001438	0. 001675547	260234	1
	BRAWH2001439	0. 162847305	86450	59
	BRAWH2001459	0. 068509233	76563	29
	BRAWH2001461	0. 047136806	76709	6
15	BRAWH2001484	0. 015770289	125985	5
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	BRAWH2001502	1. 267697555	27207	213
	BRAWH2001503	0. 001675547	285113	1
	BRAWH2001519	0. 001675547	275735	1
20	BRAWH2001530	0. 021950701	131534	6
	BRAWH2001535	0. 339353143	83177	102
	BRAWH2001589	0. 003351094	222414	2
	BRAWH2001662	0. 03644306	104160	11
	BRAWH2001666	0. 003351094	145143	2
25	BRAWH2001671	0. 044064981	135772	15
	BRAWH2001679	0. 001675547	43070	1
	BRAWH2001686	0. 001675547	208551	1
	BRAWH2001701	0. 003351094	185782	2
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30	BRAWH2001862	0. 049891555	50559	2
	BRAWH2001873	0. 001675547	199204	1
	BRAWH2001940	0. 004480285	104286	3
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35	BRAWH2002060	0. 002864792	110855	2
	BRAWH2002062	0. 003072702	168588	2

	BRAWH2002125	0. 001675547	33389	1
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5	BRAWH2002352	0. 001675547	182411	1
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	BRAWH2002630	0. 001675547	205437	1
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15	BRAWH2002725	0. 001675547	262605	1
	BRAWH2002761	0. 001675547	276467	1
	BRAWH2002811	0. 019428385	140433	8
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20	BRAWH2002963	0. 014042972	145002	3
	BRAWH2002967	0. 003757059	143402	2
	BRAWH2002976	0. 001675547	34620	1
	BRAWH2003000	0. 002864792	121508	2
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25	BRAWH2003135	0. 004796353	75904	2
	BRAWH2003240	0. 021350649	80779	4
	BRAWH2003307	0. 001675547	227712	1
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30	BRAWH2003662	0. 027035576	142685	13
	BRAWH2003689	0. 003552389	129639	2
	BRAWH2003693	0. 048975235	55559	16
	BRAWH2003818	0. 05536172	39487	11
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35	BRAWH2003948	0. 001675547	46769	1
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	BRAWH2004068	0. 001675547	60350	1
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	BRAWH2004095	0. 141739371	91975	53
5	BRAWH2004136	0. 010530678	204838	4
	BRAWH2004217	0. 003072702	79530	2
	BRAWH2004580	0. 009214721	149244	4
	BRAWH2004731	0. 001675547	172111	1
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10	BRAWH2004842	0. 042036641	125533	22
	BRAWH2004884	0. 001675547	148802	1
	BRAWH2004923	0. 001675547	251058	1
	BRAWH2005008	0. 010148342	92454	5
	BRAWH2005068	0. 416566647	145643	23
15	BRAWH2005074	0. 004771043	99951	2
	BRAWH2005225	0. 028905305	140646	10
	BRAWH2005315	0. 001675547	117854	1
	BRAWH2005517	0. 003757059	47957	2
	BRAWH2005524	0. 001675547	150027	1
20	BRAWH2005533	0. 001675547	275384	1
	BRAWH2005578	0. 012503372	158656	7
	BRAWH2005661	0. 104812185	103899	29
	BRAWH2005812	0. 001675547	92953	1
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25	BRAWH2005998	0. 005519631	165543	2
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	BRAWH2006450	0. 033369032	128986	13
	BRAWH2006493	0. 032942226	142646	13
	BRAWH2006526	0. 003072702	192799	2
35	BRAWH2006543	0. 038198657	124033	19
	BRAWH2006622	0. 010126419	112961	4

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	BRAWH2006960	0. 001675547	42476	1
	BRAWH2006989	0. 006708875	161487	3
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5	BRAWH2007069	0. 001675547	173997	1
	BRAWH2007308	0. 003351094	108276	2
	BRAWH2007406	0. 001675547	196415	1
	BRAWH2007550	0. 001675547	161434	1
	BRAWH2007570	0. 001675547	78177	1
10	BRAWH2007591	0. 0533923	82609	32
	BRAWH2007605	0. 081686424	109624	37
	BRAWH2007658	0. 014419301	158117	6
	BRAWH2007664	0. 016375786	30706	5
	BRAWH2007800	0. 071331673	110609	8
15	BRAWH2007808	0. 004469858	158139	3
	BRAWH2007825	0. 002864792	90359	2
	BRAWH2007862	0. 001675547	156457	1
	BRAWH2007890	0. 001675547	33980	1
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20	BRAWH2008128	0. 007588159	141840	2
	BRAWH2008219	0. 011627806	2127	4
	BRAWH2008255	0. 039660178	118528	7
	BRAWH2008292	0. 004590404	23747	2
	BRAWH2008297	0. 001675547	116427	1
25	BRAWH2008366	0. 013139493	32578	2
	BRAWH2008380	0. 001675547	221636	1
	BRAWH2008540	0. 003072702	168580	2
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30	BRAWH2008790	0. 001675547	169218	1
	BRAWH2008903	0. 039628131	86047	18
	BRAWH2008956	0. 010761144	116317	6
	BRAWH2008993	0. 003363824	110730	2
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35	BRAWH2009227	0. 010601532	157980	3
	BRAWH2009238	0. 03214183	66051	20